LENTIVIRUS VECTOR SYSTEM

FIELD

The invention relates to retroviral vectors, and their use in gene transfer.

BACKGROUND

The human immunodeficiency virus (HIV) is the etiological agent of the acquired immunodeficiency syndrome (AIDS) and related disorders. The expression of the virus in infected persons is regulated to enable the virus to evade the host's immune response. The HIV viruses (e.g. HIV-1 and HIV-2), as well as the simian immunodeficiency virus (SIV), share many structural and regulatory genes such as *gag*, *pol*, *env*, *tat*, *rev* and *nef*. See Guyader et al., *Nature* 328:662-669, 1987, which is incorporated by reference. HIV has been classified as a lentivirus because it causes slow infection, and has structural properties in common with such viruses (Haase, *Nature* 322:130-136, 1986).

All known retroviruses share features of the replicative cycle, including packaging of viral RNA into virions, entry into target cells, reverse transcription of viral RNA to form the DNA provirus, and stable integration of the provirus into the target cell genome. Replication competent proviruses contain, at a minimum, regulatory long terminal repeats (LTRs) and the *gag*, *pro*, *pol* and *env* genes which encode core proteins, a protease, reverse transcriptase/RNAse H/integrase and envelope glycoproteins, respectively.

HIV shares the *gag*, *pro*, *pol* and *env* genes with other retroviruses. HIV-1 also possesses additional genes modulating viral replication, such as the *vif*, *vpr*, *tat*, *rev*, *vpu* and *nef* genes. HIV-2 contains a *vpx* gene which is not present in HIV-1, but lacks the HIV-1 *vpu* gene. Additionally the long terminal repeats (LTR) of both HIV-1 and HIV-2 contain cis-acting sequences that are important for integration, transcription and polyadenylation.

HIV, like other retroviruses, are RNA viruses that replicate through a DNA proviral intermediate which is integrated into the genome of the infected host cell. The virion particle contains a dimer of positive strand genomic RNA molecules, which is transcribed from the proviral DNA by the host RNA polymerase II. A portion of these full length RNAs which encode the *gag* and *pol* genes of the virus are translated by the host cell ribosomes to produce the structural and enzymatic proteins required for production of virion particles. The provirus also gives rise to a variety of smaller singly and multiply spliced mRNAs coding for the envelope proteins and regulatory proteins.

Wild type retroviruses have been modified to become vehicles for the delivery, stable integration, and expression of cloned genes into a wide variety of cells for experimental and therapeutic purposes. To achieve the aims of transfer and expression of nonviral genes, the vector behaves as a retroviral genome and passes as a virus from a producer cell line. Hence its DNA

contains the regions of the wild-type retroviral genome required in *cis* for incorporation into a retroviral particle. In addition the vector also contains regulatory signals that lead to the optimization of the expression of the cloned gene once the vector is integrated in the target cell as a provirus.

All viral structural genes can be discarded and replaced by heterologous coding sequences, but certain essential sequence elements are retained within the vector. These sequence elements include the packaging sequence, a tRNA binding site, sequences in the LTR that permit "jumping" of the reverse transcriptase between RNA strands during DNA synthesis, sequences near the ends of the LTRs that are necessary for the integration of the vector DNA into the host cell chromosome, and sequences adjoining the 3' LTR that serve as the priming site for synthesis of the plus strand DNA molecules. See Rapley and Walker, Molecular Biomethods Handbook, 1998, chapter 18 for a discussion of principles of retroviral vector construction, and Lewin, Genes V, 1995, chapter 35, for a discussion of the function of retroviral genes. Since vector genomes do not require that the viral structural genes *gag*, *pol* and *env* be retained, nonviral genes can be cloned into the space vacated by their removal.

A significant advance in the use of retroviral vectors has been the use of packaging cells that stably or constitutively express the viral *gag*, *pol* and *env* genes (for example from plasmids) that cannot themselves be packaged by their own encoded proteins, because they lack the essential packaging sequences. However, when a retroviral transfer vector genome is transfected into such a packaging cell, the viral proteins recognize and package the vector RNA genome into viral particles that are released into the culture supernatant. In such a vector system, the transfer vector (which includes the packaging sequence) shuttles the transgene with the potential for regulation and high titer encapsidation, while the packaging cell line encapsidates the transfer vector RNA but not the viral RNA, so that the packaging cell line does not act as a helper virus. The viral particles produced in this manner can be used to deliver the encapsidated retroviral vector to a target cell with high efficiency.

For HIV-2, it has previously been reported that the leader sequence of this lentivirus contains a packaging signal downstream of the splice donor site (Garzino-Demo et al., *Hum. Gene Ther.* 6:177-184, 1995). Another report suggested that the downstream sequence elements made only a minor or no contribution to RNA encapsidation, and that the major element was located upstream of the splice donor site (McCann and Lever, *J. Virol.* 71:4133-4137, 1997). Since a knowledge of the packaging signals of HIV-2 is important to the optimal construction of packaging deficient vectors, this uncertainty about the location of the packaging signals has impeded the use of HIV-2 retroviral vector systems.

Moreover, it would be advantageous to express a transgene using an HIV-2 retroviral vector, in such a manner that packaging of the vector RNA is maximized, without an increase in the packaging of viral RNA.

SUMMARY

The invention derives from the discoveries that:

1) deletion of sequences both upstream and downstream of the 5' splice donor (SD) region of the HIV-2 provirus (packaging vector) results in *suppressed* encapsidation of packaging vector genomes without critical loss of gene expression, thus the production of "helper virus" is suppressed while making adequate structural viral protein available for encapsidation of foreign nucleotides; and

2) that functional deletion of the SD site of the HIV-2 provirus (transfer vector) results in *enhanced* encapsidation of the transfer vector's own genome, especially when the host cell has been co-transfected with the packaging vector as described under (1) above; and

3) that the HIV-2, but not HIV-1, packaging vector specifically and faithfully packages its own optimally constructed transfer vector as described under (2) above; and

4) that HIV-2 packaging vector gives both better quality and titer of vector.

Transfer and packaging vectors incorporating one or a combination of these features are useful as gene delivery agents, for example gene therapeutic agents, and provide an improved HIV-2 viral vector system that allows transfer of a transgene into the genome of non-dividing cells. The vectors of the invention also may be used to create a high-efficiency packaging cell line that provides greatly enhanced packaging of foreign DNA, especially when such DNA is carried within the SD deleted transfer vector of the invention. Additionally, it has been discovered that, for the transfer vector of the invention, deletion of the 3' LTR and its replacement with a puromycin-poly(A) cassette results in still further suppression of encapsidation of packaging virus genomes, without substantial loss of viral particle expression.

The invention includes the transfer vector derived from an HIV lentivirus, such as HIV-2/ST, wherein the vector is functionally deleted for the splice donor site (SD), and contains a functional packaging signal and a transgene operably linked to a promoter. When susceptible cells (such as 293 cells) are co-transfected with the transfer vector and a packaging-defective HIV-2 having a functional deletion of its packaging signal, production of progeny virions is enhanced by deletion of the SD. Alternatively, the transfer vector can be introduced into a packaging cell stably transfected with the packaging vector. In particular embodiments, the lentivirus is HIV-2, the functional deletion of SD comprises nucleotide changes and/or deletions in the SD nucleotide sequence, and the transgene is a *neo* gene.

In other embodiments, the invention includes a packaging vector derived from HIV-2, such as HIV-2(ROD), comprising a 5' splice donor site, and an upstream and a downstream packaging signal sequence in the leader sequence, wherein both the upstream and downstream packaging signal sequences are functionally deleted to substantially eliminate packaging of progeny viral RNA, but the splice donor site is functionally intact. In particular examples, the deletions in the packaging sequence comprise no more than 164 nucleotides upstream of the SD and no more than 62 nucleotides downstream of the SD, for example 153 nucleotides (nt 306-458) upstream of

the SD, and 52 nucleotides (nt 486-538) downstream of the SD. In particular examples, each deletion is at least 5, 10, 20, 50 or 100 nucleotides in length.

In other examples, the upstream packaging signal is contained in nucleotides downstream from nucleotide 300 and upstream from the SD, and the downstream packaging signal corresponds to nucleotides downstream from the SD and upstream from nucleotide 539. The packaging vector may also include a 3' LTR that is functionally deleted, for example by replacement of the 3' LTR with a heterologous transcriptional termination sequence.

In an alternative embodiment, the HIV packaging vector (or stably transfected cell) includes a polynucleotide sequence which encodes HIV proteins (such as HIV-2 proteins), wherein the polynucleotide sequence includes a mutation in a leader sequence upstream from a 5' splice donor site, and a mutation between the 5' splice donor site and an initiation codon of a gag gene, which results in HIV RNA (such as HIV-2 RNA) transcribed from the vector being substantially packaging defective. The polynucleotide sequence may include (a) a DNA segment from an HIV-2 genome, wherein the DNA segment comprises the HIV *gag*, *pol*, *rev* and *env* genes, and the vector lacks the bipartite HIV-2 packaging sequence necessary to package HIV-2 RNA into virions; (b) an intact 5' splice donor site; and (c) a promoter operably linked to the DNA segment of (a), wherein the vector, when introduced into or expressed in a eukaryotic host cell, expresses HIV-2 Gag, Pol, Rev, and Env proteins, as well as the Tat protein (if the linked promotor is 5' LTR), to form HIV-2 virions that are not packaged.

In some embodiments, the transfer vector includes a polynucleotide sequence which encodes a transgene, and an HIV (such as an HIV-2) packaging signal and promoter, but which does not encode one or more of a complete *gag*, *pol*, or *env* gene, and in which the splice donor site is mutated to render it non-functional, which increases encapsidation of the transgene vector RNA, compared to encapsidation of the transgene RNA in the absence of the mutation in the splice donor site. The splice donor site may be mutated to functionally delete it by substantially deleting the site, changing its nucleotides, or deleting a sufficient portion of it to increase encapsidation of the transgene RNA.

The invention also includes a cell that expresses or has been transfected with the transfer vector and/or the packaging vector, or which stably expresses the genome of the packaging vector. In particular examples, the cell is a 293T or SupT cell, the transfer vector is pSGT-5(SDM) and the packaging vector is pROD(SD36). When the cell is transfected with or stably expresses both the transfer and packaging vectors, transgene RNA encapsidation is substantially increased in the presence of the transfer vector with the mutated splice donor site, as compared to transgene encapsidation in the presence of the transfer vector in which the splice donor site is not mutated. In particular examples, the packaging vector is an HIV-2(ROD) clone, such as pROD(SD36) or a combination of envelope defective pROD(SD36/EM) and envelope expression plasmid pCON-ENV(ROD). In addition to parental HIV-2(ROD), HIV-2 envelope is derived from mutant HIV-2 and it can fuse with a broad variety of cells whether they contain CD4 markers or not.

Other embodiments include dividing the packaging vector functionally and structurally into two. The first vector contains all of the necessary elements of a packaging vector, except that its envelope is defective. In particular embodiments, this vector is pROD(SD36/EM) or pCM-ROD(SD36/EM). The second vector provides the envelope in trans, to complement the defect. In particular embodiments, this vector is pCM-VSV-G or pCM-ENV(ROD).

The invention also includes a method for improving encapsidation of transgene RNA using retroviral packaging and transfer vectors by (in any order) introducing into the target cell the transfer vector and packaging vector. Alternatively, the transfer vector can be introduced into a cell that stably expresses an HIV-2 packaging genome that has been rendered packaging deficient by the mutation of both the upstream and downstream packaging signals.

Also included in the invention are functionally equivalent transfer and packaging vectors generated using the SIV genome.

Also included in the invention are the supernatant of the packaging cell that includes the encapsidated vector RNA, and the encapsidated vector RNA itself.

The foregoing and other objects, features, and advantages of the invention will become more apparent from the following detailed description of several embodiments which proceeds with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. 1A-C show the restriction map of HIV-2 ROD.

FIG. 2 is a schematic comparison of the genomes of (a) HIV-1 and (b) HIV-2, showing the genomic locations of the genes in each retrovirus.

FIGS. 3A-E shows the upstream and/or downstream sequence deletions from HIV-2(ROD) that generate the following packaging vectors: (A) pROD(PK36) (SEQ ID NO 2); (B) pROD(SK36) (SEQ ID NO 3); (C) pROD(SD36) (SEQ ID NO 4); (D) pROD(CG36) (SEQ ID NO 5); and (E) pROD(MR36) (SEQ ID NO 6). Wild-type HIV-2(ROD) (Leader sequence, SEQ ID NO 1) is shown on top with the corresponding deletions for the packaging vectors below.

FIGS. 4A-E shows dividing the packaging vector into two parts. (A) The sequence of SD36/EM, which is identical to SD36 (see FIG. 3C), except that sequences (SEQ ID NO 7) have been added to the envelope region (nt 6351-6380), generating an envelope insertion mutant. Wild-type HIV2(ROD) sequence (SEQ ID NO 8) is shown on top with the corresponding insertion shown on the bottom for SD36/EM. (B-D) Sequence of the complementing vector, pCM-ENV(ROD), which contains a functional envelope (SEQ ID NO 9). (E) Combinations of transfer vector [pSGT-5(SDM)] with packaging vectors (either in one or two parts) that can be used.

FIGS. 5A-C shows the sequences for an SIV vector system. (A) The SIV 5' LTR leader sequence (SEQ ID NO 10). (B) The packaging vector pSIV(SD36) with deletions upstream and downstream from the SD (SEQ ID NO 11). (C) The transfer vector pSIV (SDM) with a mutated

SD (SEQ ID NO 12). For (B) and (C), the wild-type SIV sequence is shown on top with the deletions and/or mutations shown below.

FIGS. 6A and B show the genetic structure of several HIV-2 transfer vectors (A) without or (B) with RRE sequences. The abbreviations represent the following: LTR, long terminal repeat; SD, splice donor; IRES, independent ribosomal entry site; *neo*, neomycin-resistance gene; and RRE, Rev response element. Clone pSGT(SDM) differs from clone pSGT-5(RRE) in having a modified splice donor site, denoted by a cross in the figure, which indicates a mutated or deleted SD that increases encapsidation of the vector RNA.

FIGS. 7A-G shows the sequences of the HIV-2(ST) derived transfer vectors. Wild-type HIV-2(ST) (SEQ ID NO 13) is shown on top with the corresponding deletions in the transfer vectors below. (A-C) Transfer vector pSGT-5(SDM/RRE1) (SEQ ID NO 14). Nucleotides –534-0 correspond to the upstream U3 region of pSGT-5(SDM). Nucleotides 1-2195 correspond to the HIV-2 part of the pSGT-5(SDM) sequence. To these sequences, (D) full-length IRES and neo sequences (SEQ ID NO 15) are attached as shown schematically in FIG. 6E. The 5'LTR sequence of pSGT-5(SDM/RRE1) (SEQ ID NO 16). (F) Nucleotides 300-550 of pSGT-5(SDM) (SEQ ID NO 17) showing the substitution mutation of the SD. Wild-type SD is in italics. (G) Nucleotides 300-550 of pSGT-5(SDX) (SEQ ID NO 18) showing the deletion mutation of the SD.

FIG. 8 illustrates the effect of leader sequence deletions on the expression of HIV-2(ROD) cellular RNA (cRNA) and intracellular p27 protein (cp27) in human epitheloid 293 cells.

FIG. 9 illustrates the effect of leader sequence deletions in HIV-2(ROD) on the packaging of viral RNA (vRNA) and viral p27 protein (vp27) in human epithelioid 293 cells.

FIG. 10 illustrates the effect of leader sequence deletions on the expression of HIV-2(ROD) in human lymphoid CEM cells.

FIG. 11 illustrates the effect of leader sequence deletions on the packaging of viral RNA (vRNA) and proteins (vp27) of HIV-2(ROD) in human lymphoid CEM cells.

FIG. 12 shows a Northern assay illustrating processing of vector RNA in human epitheloid 293T cells. (a) Cotransfection with wild type HIV-2 proviral clone (pROD). RNA from cells transfected with: lane 1, pSGT-3(RN); lane 2, pSGT-5(RN); lane 3, pSGT-3(RRE); lane 4, pSGT-5(RRE), and lane 5, pSGT-3(SL). The size of the lower band in all lanes was about 2.0 Kb and that of the upper band was 2.9 Kb (lane 1), 3.2 Kb (lane 2), 3.2 Kb (lane 3), and 3.5 Kb (lane 4). (b) Co-transfection with mutant HIV-2 proviral clone pROD(SD36) (lanes 1-3) in which the splice donor site has been mutated, and HIV-1 (env⁻) (lanes 5-6). RNA from cells transfected with lanes 1, pSGT-5(RN); lane 2, pSGT-5(RRE); lane 3, pSGT-5(SDM); lane 4, pSGT-5(RRE); lane 5, pSGT(SDM); and lane 6. (c) Vector clone containing chemokine RANTES gene (lane 1) or IRES-neo (lane 2) co-transfected with wild type HIV-2 proviral clone pROD.

FIG. 13 shows the results of cross packaging experiments between HIV-1 and HIV-2 vectors.

FIG. 14 shows the genetic structure of several HIV-2 transfer vectors, where the abbreviations represent the following: LTR, long terminal repeat; gag; RRE, Rev response element; CMV, Cytomegalovirus promoter; GFP, green fluorescent protein; AADC aromatic amino acid decarboxylase; BAX; α-GAL-A, α-galactosidase; CMK, chemokine. Clone pSGT(SDM) differs from clone pSGT-5(RRE) in having a modified splice donor site, denoted by a cross in the figure, which indicates a mutated or deleted SD that increases encapsidation of the vector RNA.

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand.

SEQ ID NO 1 shows the nucleic acid sequence for the HIV-2(ROD) leader sequence.

SEQ ID NO 2 shows the nucleic acid sequence for the pROD(PK36) leader sequence.

SEQ ID NO 3 shows the nucleic acid sequence for the pROD(SK36) leader sequence.

SEQ ID NO 4 shows the nucleic acid sequence for the pROD(SD36) leader sequence.

SEQ ID NO 5 shows the nucleic acid sequence for the pROD(CG36) leader sequence.

SEQ ID NO 6 shows the nucleic acid sequence for the pROD(MR36) leader sequence.

SEQ ID NO 7 shows the nucleic acid sequence for the pROD(SD36/EM) envelope region.

SEQ ID NO 8 shows the nucleic acid sequence for the HIV-2(ROD) envelope region.

SEQ ID NO 9 shows the nucleic acid sequence for the pCM-ENV(ROD) vector.

SEQ ID NO 10 shows the nucleic acid sequence for the SIV 5' LTR leader sequence.

SEQ ID NO 11 shows the nucleic acid sequence for the pSIV(SD36) leader sequence.

SEQ ID NO 12 shows the nucleic acid sequence for the pSIV(SDM) leader sequence.

SEQ ID NO 13 shows the nucleic acid sequence for the HIV-2(ST) 5' LTR.

SEQ ID NO 14 shows the nucleic acid sequence for the transfer vector pSGT-5(SDM/RRE1).

SEQ ID NO 15 shows the nucleic acid sequence for the IRES and neo sequences within pSGT-5(SDM/RRE1).

SEQ ID NO 16 shows the nucleic acid sequence for the pSGT-5(SDM/RRE1) 5' LTR.

SEQ ID NO 17 shows nucleotides 300-550 of the pSGT-5(SDM/RRE1) region containing the substitution mutation of the SD..

SEQ ID NO 18 shows the nucleic acid sequence for pSGT-5(SDX/RRE1) leader region.

SEQ ID NO 19 shows the nucleic acid sequence for 300-nucle tide fragment of HIV-2(ST) RRE1 (nucleotides 7661-7960 of Genbank Accession No. M31113).

SEQ ID NO 20 shows the nucleic acid sequence for the transfer vector pSGT-5(RRE1), which contains a wild-type SD at nt 1023-1028.

SEQ ID NO 21 shows the nucleic acid sequence for the pROD(SD36/EM) packaging vector.

SEQ ID NO 22 shows the nucleic acid sequence for the pCM-ROD(SD36/EM) packaging vector.

SEQ ID NO 23 shows the nucleic acid sequence for the pCM-ENV(ROD) envelope vector.

SEQ ID NO 24 shows the nucleic acid sequence for RRE2, a 530-nucleotide fragment of HIV-2(ROD) (nucleotides 7617-8146 of Genbank Accession No. X05291).

SEQ ID NO 25 shows the nucleic acid sequence for the GFP (Genbank Accession No U55762).

SEQ ID NO 26 shows the nucleic acid sequence for 792-nucleotide fragment of HIV-2(ST) RRE1 (nucleotides 7462-8254 of Genbank Accession No. M31113).

SEQ ID NO 27 shows the nucleic acid sequence for the murine α-GAL-A.

SEQ ID NO 28 shows the nucleic acid sequence for the human AADC.

SEQ ID NO 29 shows the nucleic acid sequence for the human RANTES gene (nt 1-466 of Genbank Accession Number NM_002985).

SEQ ID NO 30 shows the nucleic acid sequence for human BAX (Genbank Accession No. L22474).

SEQ ID NO 31 shows the nucleic acid sequence for the backbone transfer vector, pSGT5(SDM/RRE1/CM).

SEQ ID NO 32 shows the nucleic acid sequence for the IRES and puromycin sequences

DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

Abbreviations and Definitions

The following definitions and methods are provided to better define the present invention and to guide those of ordinary skill in the art in the practice of the present invention. It must be noted that as used herein and in the appended claims, the singular forms "a" or "an" or "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a protein" includes a plurality of such proteins and reference to "the antibody" includes reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

AADC: aromatic amino acid decarboxylase

α-GAL-A: α-galactosidase

CMV: Cytomegalovirus promotor

GFP: Green fluorescent Protein

PCR: polymerase chain reaction

PMSF: Phenylmethylsulfonyl fluoride. An inhibitor of serine proteases.

RT: Room temperature

TU: Transduction units

Animal: Living multicellular vertebrate organisms, a category which includes, for example, mammals and birds.

Cancer: malignant neoplasm that has undergone characteristic anaplasia with loss of differentiation, increased rate of growth, invasion of surrounding tissue, and is capable of metastasis.

cDNA (complementary DNA): A piece of DNA lacking internal, non-coding segments (introns) and regulatory sequences which determine transcription. cDNA may be synthesized in the laboratory by reverse transcription from messenger RNA extracted from cells.

Cell lysate: A mixture resulting from the decomposition, breakdown or lysis of cells or tissue.

Deletion: The removal of a sequence of DNA. The regions on either side may be joined together, or another sequence inserted between them.

DNA: Deoxyribonucleic acid: DNA is a long chain polymer which comprises the genetic material of most living organisms (some viruses have genes comprising ribonucleic acid, RNA). The repeating units in DNA polymers are four different nucleotides, each of which comprises one of the four bases, adenine, guanine, cytosine and thymine bound to a deoxyribose sugar to which a phosphate group is attached. Triplets of nucleotides, referred to as codons, in DNA molecules code for amino acid in a polypeptide. The term codon is also used for the corresponding (and complementary) sequences of three nucleotides in the mRNA into which the DNA sequence is transcribed.

ELISA: Enzyme-linked immunosorbent assay. A form of quantitative immunoassay based on the use of antibodies (or antigens) that are linked to an insoluuble carrier surface, which is then used to capture the relevant antigen (or antibody) in the test solution. The antigen-antibody complex is then detected by measuring the activity of an appropriate enzyme that had previously been covalently attached to the antigen (or antibody).

Functional Deletion: A mutation in a sequence that has an effect equivalent to deletion of the sequence, for example eliminating the function of a packaging signal or splice donor site by a deletion, insertion, or substitution.

Functionally Equivalent: Sequence alterations, in either the transfer or packaging vector sequences, that yield the same results as described herein. Such sequence alterations can include,

but are not limited to, conservative substitutions, deletions, mutations, frameshifts, and insertions. In the packaging vector, deletions upstream and downstream from the SD which allow expression, but not encapsidation of the viral RNA as described in EXAMPLES 1 and 2, are functionally equivalent to the packaging vector of the invention. Furthermore, these deletions will not allow for the production of helper virus. In the transfer vector, alterations of the SD sequence which yield enhanced encapsidation of the transfer vector genome, especially when the transfected cell is co-transfected with a packaging vector of the invention (as described in EXAMPLE 5), are functionally equivalent to the transfer vector of the invention.

Infective: A virus or vector is "infective" when it transduces a cell, replicates, and (without the benefit of any complementary virus or vector) spreads progeny vectors or viruses of the same type as the original transducing virus or vector to other cells in an organism or cell culture, where the progeny vectors or viruses have the same ability to reproduce and spread throughout the organism or cell culture. Thus, for example, a nucleic acid encoding an HIV particle is not infective if the nucleic acid cannot be packaged by the HIV particle (e.g. if the HIV particle lacks an HIV packaging site), even though the nucleic acid can be used to transfect and transform a cell. Similarly, an HIV nucleic acid packaged by an HIV particle is not infective if it does not encode the HIV particle that it is packaged in.

Isolated: An "isolated" biological component (such as a nucleic acid, peptide or protein) has been substantially separated, produced apart from, or purified away from other biological components in the cell of the organism in which the component naturally occurs, i.e., other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids, peptides and proteins which have been "isolated" thus include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids, peptides and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

Lentivirus: Lentiviruses are characterized by long incubation periods between infection of the host and the manifestation of clinical disease. Lentiviruses infect a wide variety of mammals, including humans, monkeys, sheep, goats, and horses. Includes for example retroviruses, such as immunodeficiency viruses, such as HIV-1, HIV-2, FIV, and SIV.

Malignant: cells which have the properties of anaplasia invasion and metastasis.

Mammal: This term includes both human and non-human mammals. Similarly, the terms "subject," "patient," and "individual" includes human and veterinary subjects.

Neoplasm: abnormal growth of cells

Normal cells: Non-tumor, non-malignant cells.

Nucleic acid: A deoxyribonucleotide or ribonucleotide polymer in either single or double stranded form, and unless otherwise limited, encompasses known analogues of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally occurring nucleotides.

Olig nucleotide: A linear polynucleotide sequence of up to about 200 nucleotide bases in length, for example a polynucleotide (such as DNA or RNA) which is at least 6 nucleotides, for example at least 15, 50, 100 or even 200 nucleotides long.

Operably linked: A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame.

ORF (open reading frame): A series of nucleotide triplets (codons) coding for amino acids without any termination codons. These sequences are usually translatable into a peptide.

Ortholog: two nucleotide sequences are orthologs of each other if they share a common ancestral sequence, and diverged when a species carrying that ancestral sequence split into two species. Orthologous sequences are also homologous sequences.

Packaging cell: A cell that provides packaging functions in *trans* for a transgene introduced into a cell with a transfer vector, but which does not encapsidate its own viral RNA.

Packaging defective: A packaging vector which lacks the nucleic acids necessary for packaging of an RNA corresponding to the packaging vector nucleic acid into a retroviral (e.g. HIV, SIV) capsid. That is, packaging vector nucleic acids are not themselves encapsidated in the HIV or SIV particles which they encode, i.e. they are not infective.

Packaging signal: Nucleic acid sequences upstream and downstream from the SD which are necessary for the efficient packaging of the vector RNA genome.

Packaging vector: Packaging vector nucleic acids lack the nucleic acids necessary for packaging of an RNA corresponding to the packaging vector nucleic acid into a retroviral (e.g. HIV, SIV) capsid. That is, packaging vector nucleic acids are not themselves encapsidated in the HIV or SIV particles which they encode, i.e. they are not infective. The packaging vector optionally includes all of the components necessary for production of HIV or SIV particles, or optionally includes a subset of the components necessary for HIV or SIV packaging. For instance, a packaging cell may be transformed with more than one packaging vector, each of which has a complementary role in the production of an HIV or SIV particle.

Two (or more) HIV- or SIV-based packaging vectors are "complementary" when they together encode all of the functions necessary for HIV or SIV packaging, and when each individually does not encode all of the functions necessary for packaging. For example, when two vectors transduce a single cell and together they encode the information for production of HIV or SIV packaging particles, the two vectors are "complementary." The use of complementary vectors increases the safety of any packaging cell made by transformation with a packaging vector by reducing the possibility that a recombination event will produce an infective virus.

Packaging vectors encode HIV or SIV particles. The HIV particles are competent to package target RNA which has an HIV packaging site. The SIV particles are competent to package target RNA which has an SIV packaging site.

PCR: polymerase chain reaction. Describes a technique in which cycles of denaturation, annealing with primer, and then extension with DNA polymerase are used to amplify the number of copies of a target DNA sequence.

Pharmaceutically acceptable carriers: The pharmaceutically acceptable carriers useful in this invention are conventional. Remington's Pharmaceutical Sciences, by E. W. Martin, Mack Publishing Co., Easton, PA, 15th Edition (1975), describes compositions and formulations suitable for pharmaceutical delivery of the lentiviral vectors herein disclosed.

In general, the nature of the carrier will depend on the particular mode of administration being employed. For instance, parenteral formulations usually comprise injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, glycerol, ethanol, sesame oil, combinations thereof, or the like, as a vehicle. The carrier and composition can be sterile, and the formulation suits the mode of administration. For solid compositions (e.g., powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, sodium saccharine, cellulose, magnesium carbonate, or magnesium stearate. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides.

Probes and primers: Nucleic acid probes and primers may readily be prepared based on the nucleic acid sequences provided by this invention. A probe is an isolated nucleic acid attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed, e.g., in Sambrook et al., in Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press (1989) and Ausubel et al., in Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley-Intersciences (1987).

Primers are short nucleic acids, such as DNA oligonucleotides 15 nucleotides or more in length. Primers may be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for

amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods known in the art.

Methods for preparing and using probes and primers are described, for example, in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989), Ausubel et al., 1987, and Innis et al., PCR Protocols, A Guide to Methods and Applications, 1990, Innis et al. (eds.), 21-27, Academic Press, Inc., San Diego, California. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, © 1991, Whitehead Institute for Biomedical Research, Cambridge, MA). One of skill in the art will appreciate that the specificity of a particular probe or primer increases with its length. Thus, for example, a primer comprising 20 consecutive nucleotides of the human AADC cDNA or gene will anneal to a target sequence such as an AADC gene homolog (such as the mouse AADC gene) contained within a cDNA or genomic DNA library with a higher specificity than a corresponding primer of only 15 nucleotides. Thus, in order to obtain greater specificity, probes and primers may be selected that comprise 20, 25, 30, 35, 40, 50 or more consecutive nucleotides of the AADC cDNA or gene sequences.

The invention thus includes isolated nucleic acid molecules that comprise specified lengths of the disclosed gene sequences. Such molecules may comprise at least 20, 21, 25, 30, 35, 40, 50 or 100 or more consecutive nucleotides of these sequences and may be obtained from any region of the disclosed sequences. By way of example, the cDNA and gene sequences may be apportioned into halves or quarters based on sequence length, and the isolated nucleic acid molecules may be derived from the first or second halves of the molecules, or any of the four quarters. In particular, the DNA sequences may code for a unique portion of the protein, which has not been previously disclosed.

pROD or pSGT clone: A clone derived from a publicly available HIV-2 ROD or HIV-2 ST genomic clone, respectively, by standard recombinant techniques such as subcloning, site-directed mutagenesis and the like, or alternatively an artificial nucleic acid synthesized based upon the genomic sequence.

Promoter: A promoter is an array of nucleic acid control sequences which direct transcription of a nucleic acid. A promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements which can be located as much as several thousand base pairs from the start site of transcription. Examples of promotors includes, but is not limited to: the internal promotor CMV; LTR (long terminal repeat); inducible promoters such as the MMTV promoter and the metallothionein promoter; heat shock promoters; the albumin promoter; the histone promoter; TK promoters; B19 parvovirus promoters; and the ApoAI promoter.

Purified: the term purified does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified AADC protein preparation is one in which the protein is more pure than the protein in its natural environment within a cell. In one embodiment, a preparation of an AADC protein is purified such that the protein represents at least 50% of the total protein content of the preparation.

Recombinant: A recombinant nucleic acid is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques.

Sequence identity: The similarity between two nucleic acid sequences, or two amino acid sequences, is expressed in terms of the similarity between the sequences, otherwise referred to as sequence identity. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs or orthologs of proteins and corresponding cDNA sequences, for example of the AADC gene, will possess a relatively high degree of sequence identity when aligned using standard methods. This homology will be more significant when the orthologous proteins or cDNAs are derived from species which are more closely related (e.g., human and chimpanzee sequences), compared to species more distantly related (e.g., human and *C. elegans* sequences).

Typically, orthologs are at least 50% identical at the nucleotide level and at least 50% identical at the amino acid level when comparing human sequences, for example when comparing the AADC or RANTES sequences to orthologous AADC and/or RANTES sequences. The orthologs may be at least 60%, 70%, 80%, 90%, 95% or 98% identical at the nucleotide level.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988; Higgins & Sharp, *Gene*, 73:237-44, 1988; Higgins & Sharp, *CABIOS* 5:151-3, 1989; Corpet et al., *Nuc. Acids Res.* 16:10881-90, 1988; Huang et al. *Computer Appls. in the Biosciences* 8, 155-65, 1992; and Pearson et al., *Meth. Mol. Bio.* 24:307-31, 1994. Altschul et al,. *J. Mol. Biol.* 215:403-10, 1990, presents a detailed consideration of sequence alignment methods and homology calculations.

The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al. *J. Mol. Biol.* 215:403-10, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. It can be accessed at http://www.ncbi.nlm.nih.gov/BLAST/. A description of how to determine sequence identity using this program is available at http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html.

Homologs of the disclosed HIV and/or transgene proteins typically possess at least 60%, 70%, 75%, 80%, 90%, 95%, 98% or at least 99% sequence identity counted over full-length alignment with the amino acid sequence of the HIV and/or transgene protein using the NCBI Blast 2.0, gapped blastp set to default parameters. For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequence will show increasing percentage identities when assessed by this method, such as at least 70%, 75%, 80%, 90%, 95%, 98%, or 99% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs will typically possess at least 75% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85% or at least 90% or 95% depending on their similarity to the reference sequence. Methods for determining sequence identity over such short windows are described at http://www.ncbi.nlm.nih.gov/BLAST/blast_FAQs.html.

Alternatively, one may manually align the sequences and count the number of identical amino acids in the original sequence and a reference sequence that is compared to the original sequence. This number of identical amino acids is divided by the total number of amino acids in the reference sequence and multiplied by 100 to result in the percent identity.

One of ordinary skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided. The present invention provides not only the peptide homologs that are described above, but also nucleic acid molecules that encode such homologs.

One indication that two nucleic acid sequences are substantially identical is that the polypeptide which the first nucleic acid encodes is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

An alternative indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions, as described in EXAMPLE 21.

The present invention provides not only the peptide homologs that are described above, but also nucleic acid molecules that encode such homologs.

Sample: Includes biological samples containing genomic DNA, RNA, or protein obtained from cells, such as those present in peripheral blood, urine, saliva, tissue biopsy, surgical specimen, amniocentesis samples and autopsy material.

Specifically hybridizable and specifically complementary: Terms which indicate a sufficient degree of complementarity such that stable and specific binding occurs between the oligonucleotide (or its analog) and the DNA or RNA target. The oligonucleotide or oligonucleotide analog need not be 100% complementary to its target sequence to be specifically hybridizable. An oligonucleotide or analog is specifically hybridizable when binding of the oligonucleotide or analog to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA, and there is a sufficient degree of complementarity to avoid non-specific binding of the oligonucleotide or analog to non-target sequences under conditions in which specific binding is desired, for example under physiological conditions in the case of *in vivo* assays. Such binding is referred to as "specific hybridization." See EXAMPLE 21 for hybridization conditions.

Splice Donor Site (SD): A site in the nucleic acid sequence which is used in conjunction with a splice acceptor site elsewhere in the genome to eliminate (splice out) a segment of RNA which is not a part of the mature, functional RNA. As used herein, the splice donor site is the major splice donor used to produce all viral messages (functional RNAs coding for the proteins) except the gag-pol precursor. In the infectious full length HIV-2, this site is essential for RNA processing which is quite complex in lenitviruses and without it, virus is not replicative or infectious.

The sequence of the SD is conserved in HIV-2's and differs slightly from HIV-1. Generally, these sequence elements form a consensus set:

Consensus: Donor Exon-AG|GT AAGT--------CAG|N-Exon Acceptor

HIV-2 (ST)	GTGAAG|GTAAGT
HIV-2 (ROD)	GTGAAG|GTAAGT
HIV-1 (HXb)	CGACTG|GTGAGT
HIV-1 (89.6)	CGACTG|GTGAGT

Subject: Living multicellular vertebrate organisms, a category which includes, both human and veterinary subjects for example, mammals, birds and primates.

Sufficient complementarity: When used, indicates that a sufficient number of base pairs exist between the oligonucleotide and the target sequence to achieve detectable binding, and disrupt expression of gene products (for example the transgenes described herein). When expressed or measured by percentage of base pairs formed, the percentage complementarity that fulfills this goal can range from as little as about 50% complementarity to full, (100%) complementary. In general, sufficient complementarity is at least about 50%. However, sufficient complementarity can be least about 75%, 90%, 95%, 98% or 100% complementarity.

A thorough treatment of the qualitative and quantitative considerations involved in establishing binding conditions that allow one skilled in the art to design appropriate oligonucleotides for use under the desired conditions is provided by Beltz et al. *Methods Enzymol* 100:266-285, 1983, and by Sambrook et al. (ed.), Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

Supernatant: The culture medium in which a cell is grown. The culture medium includes material from the cell, including HIV viral particles which bud off from the cell membrane and enter the culture medium.

Therapeutically active molecule: A molecule that has a biological effect in the treatment of a pathological condition. An example of such a molecule is one which induces Fabry cells to clear excess glycolipd. Another example of such a molecule is one which induces neural cells, such as those of a Parkinson's patient, to convert L-dopa to L-dopamine. Examples of nucleic acid-based therapeutically active molecules are, but are not limited to, lentiviral vectors which express functional α-GAL-A, AADC, BAX, or chemokine proteins or fragments thereof. Therapeutically active molecules also include gene therapy vectors, such as lentiviral vectors containing therapeutic transgene nucleic acid sequences.

Transduced and Transformed: A virus or vector "transduces" a cell when it transfers nucleic acid into the cell. A cell is "transformed" by a nucleic acid transduced into the cell when the DNA becomes stably replicated by the cell, either by incorporation of the nucleic acid into the cellular genome, or by episomal replication. As used herein, the term transformation encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, calcium-DNA precipitates, and particle gun acceleration.

Transfer/Transducing vector: A vector which shuttles a transgene.

Transformed: A transformed cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. As used herein, the term transformation encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Transgene: An exogenous gene supplied by a vector. Examples of such genes include, but are not limited to: neo, GFP, AADC, α-gal, BAX or a chemokine.

Transgenic Cell: Transformed cells which contain foreign, non-native DNA.

Tumor: a neoplasm

Upstream and Downstream Sequences: Upstream sequences are those 5' to the sequence of interest and downstream sequences are 3' to the sequence of interest.

Variants of Amino Acid and Nucleic Acid Sequences: The production of proteins can be accomplished in a variety of ways. DNA sequences which encode for the protein, or a

fragment or variant of the protein, can be engineered such that they allow the protein to be expressed in eukaryotic cells, bacteria, insects, and/or plants. In order to accomplish this expression, the DNA sequence can be altered and operably linked to other regulatory sequences. The final product, which contains the regulatory sequences and the therapeutic protein, is referred to as a vector. This vector can then be introduced into the eukaryotic cells, bacteria, insect, and/or plant. Once inside the cell the vector allows the protein to be produced.

One of ordinary skill in the art will appreciate that the DNA can be altered in numerous ways without affecting the biological activity of the encoded protein. For example, PCR may be used to produce variations in the DNA sequence which encodes AADC. Such variants may be variants that are optimized for codon preference in a host cell that is to be used to express the protein, or other sequence changes that facilitate expression.

Two types of cDNA sequence variant may be produced. In the first type, the variation in the cDNA sequence is not manifested as a change in the amino acid sequence of the encoded polypeptide. These silent variations are simply a reflection of the degeneracy of the genetic code. In the second type, the cDNA sequence variation does result in a change in the amino acid sequence of the encoded protein. In such cases, the variant cDNA sequence produces a variant polypeptide sequence. In order to optimize preservation of the functional and immunologic identity of the encoded polypeptide, any such amino acid substitutions may be conservative. Conservative substitutions replace one amino acid with another amino acid that is similar in size, hydrophobicity, etc. Such substitutions generally are conservative when it is desired to finely modulate the characteristics of the protein. Examples of amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions include: Ser for Ala; Lys for Arg; Gln or His for Asn; Glu for Asp; Ser for Cys; Asn for Gln; Asp for Glu; Pro for Gly; Asn or Gln for His; Leu or Val for Ile; Ile or Val for Leu; Arg or Gln for Lys; Leu or Ile for Met; Met, Leu or Tyr for Phe; Thr for Ser; Ser for Thr; Tyr for Trp; Trp or Phe for Tyr; and Ile or Leu for Val.

Variations in the cDNA sequence that result in amino acid changes, whether conservative or not, are minimized to enhance preservation of the functional and immunologic identity of the encoded protein. The immunologic identity of the protein may be assessed by determining whether it is recognized by an antibody to AADC (or other protein of interest); a variant that is recognized by such an antibody is immunologically conserved. In particular embodiments, any cDNA sequence variant will introduce no more than 20, for example fewer than 10 amino acid substitutions into the encoded polypeptide. Variant amino acid sequences can, for example, be 80%, 90% or even 95% identical to the native amino acid sequence.

Conserved residues in the same or similar proteins from different species can also provide guidance about possible locations for making substitutions in the sequence. A residue which is highly conserved across several species is more likely to be important to the function of the protein than a residue that is less conserved across several species.

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector may include nucleic acid sequences that permit it to replicate in the host cell, such as an origin of replication. A vector may also include one or more selectable marker genes and other genetic elements known in the art. A vector can transduce, transform or infect a cell, thereby causing the cell to express nucleic acids and/or proteins other than those native to the cell. A vector optionally includes materials to aid in achieving entry of the nucleic acid into the cell, such as a viral particle, liposome, protein coating or the like.

Variant Lentiviral or Transgene peptides: Lentiviral or transgene peptides having one or more amino acid substitutions, one or more amino acid deletions, and/or one or more amino acid insertions, so long as the peptide retains the properties of the wild-type protein. Conservative amino acid substitutions may be made in at least 1 position, for example 2, 3, 4, 5 or even 10 or more positions, as long as the peptide retains the ability to function as a lentiviral or transgene protein disclosed in the present specification. For example, variants of the transgene α-GAL-A can be expressed by the lentiviral system of the present invention. Variant α-GAL-A molecules will retain the ability to be expressed by the lentiviral system at levels above that observed in Fabry fibroblasts using methods described in EXAMPLE 11. In addition, the variant α-GAL-A molecules will retain the ability clear excess lipid deposited in Fabry fibroblasts at a better rate than observed for untransduced Fabry fibroblasts, using the methods described in EXAMPLE 11.

Additional definitions of terms commonly used in molecular genetics can be found in Benjamin Lewin, *Genes V* published by Oxford University Press, 1994 (ISBN 0-19-854287-9); Kendrew et al (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0-632-02182-9); and Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 1-56081-569-8).

GENERAL METHODS

The methods of the invention are generally directed to the production of HIV derived transfer and packaging vectors which can be used (either together or in conjunction with other transfer and packaging vectors) to produce packaged transfer vectors that can be used to transfer a transgene into a target cell substantially without the production of competent pathogenic or infectious viral particles.

The present invention utilizes standard laboratory practices for the cloning, manipulation and sequencing of nucleic acids, purification and analysis of proteins and other molecular biological and biochemical techniques, unless otherwise stipulated. Such techniques are explained in detail in standard laboratory manuals such as Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989, and Ausubel et al., in Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley-Intersciences (1987).

Although the virus from which the transfer and packaging vectors are derived is an RNA virus (HIV-2 or SIV), the molecular cloning may be done using proviral DNA clones, thus allowing the use of standard cloning techniques.

Vector Construction

The packaging and transfer vectors of the invention may be derived, using standard genetic engineering techniques, from a provirus clone of a retrovirus, such as an immunodeficiency virus, for example the Human Immunodeficiency Virus, including HIV-1 or HIV-2, or the Simian Immunodeficiency Virus, SIV.

The Packaging Vector

In this example with HIV-2, it is shown that nucleotide sequences upstream and downstream of the 5' splice donor (SD) site are necessary for the efficient packaging of the vector RNA genome. Selective deletion of these essential packaging sites (packaging sequences) renders the vector incapable of packaging its own RNA (so that it is a "packaging vector"). The packaging vector in this example is made by deleting the HIV-2 packaging site both upstream and downstream of SD in HIV-2, and may be derived by genetic engineering of a provirus. The resulting deletion clones can be used to make viral particles, by transducing the deletion clone into a packaging cell and expressing the clone. Because the clones lack the HIV-2 packaging site, they are not packaged into the viral particles. To increase safety of the transduced packaging cells, the deletion clone (or homologous clones) may be cut (e.g. by subcloning) into multiple expression clones with complementary functions. This decreases the chances that a recombinant event will result in an infectious particle.

A convenient and well-defined provirus that may be used for this purpose is the provirus molecular clone (pROD1), from HIV-2 ROD (the sequence of which is available under Genbank accession no. M15390, and is further described in Arya et al., *J. Acquir. Immune. Defic. Syndr.* 6:1205-1211, 1993; Arya et al., *J. Gen. Virol.* 75:2253-2260, 1994; and Arya et al., *Hum. Gene Ther.* 9:1371-1380, 1998). Other retroviral provirus constructs may also be used, for instance an HIV-1 or SIV provirus. The sequences for these proviruses are available on Genebank at http://www.ncbi.nlm.nih.gov/Entrez/. Examples include, but are not limited to: Genbank Accession Nos. AF075702 (HIV-1 isolate SE8603 from Uganda), M17449 (HIV-1 isolate MN) and AF131870 (SIV). Such a provirus (or combination of complementary viruses), used to produce the packaging vector, should contain a substantially complete retroviral genome including the *gag*, *pol,* and *env* genes, a leader sequence and the 3' and 5' LTRs, and may contain the other HIV-2 structural genes shown in FIG. 2.

Deletions may be introduced using standard restriction vectors at appropriate sites. Sites may be selected using a restriction map of the pROD sequence (FIG. 1). Restriction may be done

upon the provirus *in situ*, or for convenience, fragments of the pROD proviral vector that contain the SD and surrounding sequence, may be subcloned into a plasmid vector. The inserted nucleotides in such a subclone may be restricted or altered as desired, and then reinserted into an appropriately modified pROD clone. Clones thus constructed may then be confirmed by DNA sequencing.

The packaging vector thus produced will not be able to package its own genome, and is therefore not infective, but it will be able to package the genome of another virus that possesses the wild-type packaging sequence(s), for example, the transfer vector of the invention. The packaging vector may optionally be surrounded by a capsid to comprise a viral particle. The engineered proviral DNA packaging vector can be used to co-transfect cultured mammalian (e.g., human) cells *in vitro* or to produce a packaging cell line, as discussed below.

In another example, the packaging vector can be functionally and structurally divided into two parts. One part will be as described above, that is it will contain deletions upstream and downstream of the SD. In addition, it will also contain mutations or deletions which prevent the production of an envelope. The second part will provide the envelope only, thereby complementing the first.

The Transfer Vector

A transfer vector in this example is a nucleotide construct that delivers a transgene (for example a non-native gene) into a target cell. The transgene is then generally integrated into the genome of the target cell where it is expressed. The transfer vector contains the nucleotide sequences required for efficient packaging of its RNA genome (including the transgene) and can be made from an HIV-2 proviral clone, such as, for example, HIV-2/ST (Genbank Accession no. M31113, Kumar et al., *J. Virol.* 64:890-901, 1990, which discloses the complete sequence of HIV-2/ST; Arya et al., *J. Acquir. Immune. Defic. Syndr.* 6:1205-1211, 1993; Arya et al., *AIDS Res. Human. Retroviruses.* 9:839-48, 1993). Alternatively, the transfer vector of the invention can be derived from the provirus of another retrovirus such as HIV-1 or SIV. Standard genetic engineering techniques can be used to manipulate the proviral genome.

In this example, it is illustrated that functional deletion of the SD site in the proviral genome of HIV-2 dramatically increases the encapsidation of the transfer vector genome, especially when the transfected cell is co-transfected with a packaging vector of the invention. This discovery is significant because it provides a retroviral packaging system with significantly enhanced packaging of transfer vector RNA and significantly reduced packaging of packaging vector RNA. These are important features for any retroviral gene therapy vector to have, particularly if the retroviral vector is derived from a pathogenic virus.

The SD portion of the genome can be functionally deleted in many ways. For example, the SD can be functionally deleted by changing the nucleotide sequence, by physical excision of all or part of the SD sequence, by a frameshift mutation, or by introduction of a foreign gene

sequence within the SD sequence, for instance, a foreign gene sequence carrying a reporter molecule. Functional deletion also includes use of substitution mutants which disrupt the function of the SD, or any other mutation that disrupts the SD and enhances packaging of progeny transfer vector genomes. This effect is enhanced when the transfected cell is co-transfected with a packaging-defective packaging vector such as described herein. For instance, when human 293 cells are transfected with the transfer vector functionally deleted for SD and co-transfected with a packaging-defective HIV-2 genome, packaging of progeny transfer genomes is enhanced (for example by a factor of at least 2, 5, 10, 20 or even 30) in comparison to a co-transfection wherein the transfer vector is not deleted for SD.

A transfer vector can generally further possess a packaging signal and a transgene operably linked to a promoter. The transgene can be any gene that would provide an advantage if delivered to a target cell. Examples of transgene include, but are not limited to: cytosine deaminase in a subject suffering from SCID (severe combined immuno-deficiency syndrome); HSV-TK in a subject having a tumor that is to be treated by the administration of ganciclovir; AADC in a subject suffering from Parkinson's disease; α-GAL-A in a subject suffering from Fabry disease; or a cytokine to a patient suffering from an infectious disease such as AIDS. The promoter for such a transgene can include promoters that can be regulated by an inducer or repressor, promoters that are constitutive, or promoters that show cell-type specificity. For example, the 5' HIV LTR promoter can be used that is induced in response to HIV infection. Such a promoter would be particularly useful if the transgene encoded a product that provided a treatment against HIV infection. Cell-type specific promoters can be advantageous for the treatment of various cancers, linked to an anti-tumor agent such as the herpes simplex virus thymidine kinase gene (HSV-TK). For example, the albumin and alpha-fetoprotein promoters tend to be liver-specific; the carbonic anhydrase I promoter is specific for colon cells; the prostate-specific antigen promoter is specific for prostate cells, and the villin, glucagon and insulin promoters are specific for pancreatic cells. Thus, linking an HSV-TK gene to a cell-type specific promoter would encourage expression of HSV-TK in the specific tissue targeted. In addition, the heterologous cytomegalovirus (CMV) promotor can also be used to allow the system to be used in a wide variety of cell types.

A transfer vector so constructed can be used to transfect cultured mammalian cells or producer cells co-transfected with a packaging vector, thus producing encapsidated transfer vector genomes that could be used to transfer a transgene into a target cell. The type of target cell susceptible to infection with such progeny virus will be dependent on the type of virus from which the packaging vector is derived, because infectivity is determined by the envelope proteins of the virus.

Cell Transfecti n To Pr duce Packaged Transfer Virus

The transfer and packaging vectors constructed as described herein can be used to transfect mammalian cells. Examples of cells that can be transfected include, but are not limited to: human epitheloid 293 or 293T cells, human lymphoid CEM cells, human SupT cells, human HeLa cells (ovarian epitheloid ATCC #CCL-2) human fresh PBMC cells (lymphocytes), human monocytic cells, such as U937 cells, human fibroblasts (such as HS27, ATCC # CRL-1634), normal human skin fibroblasts CD-27sk (ATCC # CRL-1475), fetal brain cells (such as SVG (ATCC #CRL-8621), HFGC cells, and SVG-neural differentiated cells), glimoa cells (such as U281 and U373, ATCC # HTB-17) and human neuroblastoma cells (such as SKN-MC, ATCC # HTB-10 and SKN-SH). Such transfection will result in the production of a packaged transfer vector that can be used to transduce a target cell and thereby transfer a transgene into the genome of the target cell.

Transfection can be performed by routine methods whereby naked nucleic acids are transferred across the cell membrane thereby entering the interior of the cell where the proviral DNA can be subject to transcription and translation using the host's cellular machinery. For example, the naked proviral DNA can be transfected into the cell using the well-known calcium phosphate transfection method (see for example, EXAMPLE 9 and Arya et al., *AIDS Res. Hum. Retrovirus*. 9:839-48, 1993; Arya et al., *J. Acquir. Immune. Defic. Syndr.* 6:1205-1211, 1993). The conditions for transfection can be varied widely, for instance with regard to the amount of DNA applied and the components used in the medium to make the host cell membrane permeable to the naked DNA. The cells and supernatant from such a transfected cell culture can be harvested after a few days, for example 3-5 days. Such transfected cell cultures can be examined visually for syncytial formation, indicative of cytopathy. The number of virus particles in the supernatant can be estimated by the standard antigen capture assay scoring for the p27 core protein. Such methods are discussed, for example in EXAMPLES 1 and 2, and Arya et al., *Proc. Natl. Acad. Sci. USA*. 93:4486-4491, 1996 and in Al-Harthi et al., *AIDS Res. Hum. Retroviruses* 14:59-64, 1998.

Cells can also be transfected using DEAE-dextran (Arya, *New Bio.* 2:57-65, 1990; Arya and Sethi, *AIDS Res. Hum. Retroviruses*. 6:649-658, 1990), lipofectamine (as per the manufacture's instructions, GIBCO-BRL, Gaithersburg, MD) or any other method used by those skilled in the art.

Production Of Packaging Cell Lines

The packaging vector(s) of the invention can be used to produce a high efficiency packaging cell line. The packaging vector lacks nucleic acids required to package its own genome, but when introduced into a cell co-transfected with a transfer vector (or any virus that carries the wild-type packaging sequence), the transfer vector RNA genome will be packaged, resulting in

virus particles capable of infecting target cells and transferring a transgene into such target cells. Such packaging cell lines can be derived from many cell types including, but not limited to, the HeLa cell line, human lymphoid cell lines (e.g., CEM cells), human embryonic kidney (HEK) cells such as 293 cells, or for example the cell lines listed above and described in EXAMPLE 10. Other techniques for making packaging cell lines are disclosed in PCT/US97/05272. Once stable transformed cell lines are made which express the lentiviral particles (for example HIV-1, HIV-2 or SIV), the transformed cell lines are transfected with the transfer vectors, which encode transgenes.

Infection Of Target Cells By Progeny Virus

Target cells can be infected under standard culture conditions by the progeny virus of the invention. Target cells can be any cell type susceptible to infection by the virus from which the packaging vector was derived. For example, if the packaging vector is derived from HIV-2, the target cells can be lymphocyte cells such as $CD4^+$ T cells or macrophages. Progeny virus will be present in cell-free supernatants of infected producer cell cultures. This supernatant can be used as a source of progeny virus, and when target cells, for instance a monolayer of $CD4^+$ cells, are exposed to this supernatant, infection will occur within a few hours, for example 2-4 hours. After about five days, infected cells will display syncytia formation. The supernatant from these infected cells can be harvested for analysis and secondary virus production can be evaluated by p27 core antigen capture assays as described herein.

Analysis of Transgene Expression

Expression of the transgene in transfected cells can be evaluated by a variety of techniques including ELISA, Northern blot and other standard protein assays which allow one to determine that the transgene is being expressed (for example assaying for the conversion of L-dopa to L-dopamine after transfecting cells with the AADC gene). Transfected cells can be analyzed for cellular RNA by extraction of the RNA by standard methods, and by measurement of absorbance of light at set wavelengths. Northern blot and slot-blot hybridization can be used to quantify RNA.

Clones with Equivalent Nucleic Acids

Given the strategy for making the packaging and target packageable nucleic acids of the present invention, one of skill can construct a variety of clones containing functionally equivalent nucleic acids. Cloning methodologies to accomplish these ends, and sequencing methods to verify the sequence of nucleic acids are well known in the art. Examples of appropriate cloning and sequencing techniques, and instructions sufficient to direct persons of skill through many cloning exercises, are found in Berger and Kimmel, *Methods Enzymol* 152:307-16 (1987); Sambrook et

al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989, and Ausubel et al., in Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley-Interssciences (1987).

The nucleic acid compositions of this invention, whether RNA, cDNA, genomic DNA, or a hybrid of the various combinations, are isolated from biological sources or synthesized *in vitro*. The nucleic acids of the invention are present in transformed or transfected whole cells, in transformed or transfected cell lysates, or in a partially purified or substantially pure form.

One skilled in the art will appreciate that many conservative variations of the nucleic acid constructs disclosed yield a functionally identical construct. For example, due to the degeneracy of the genetic code, silent variations (substitutions of a nucleic acid sequence which do not result in an alteration in an encoded polypeptide) are an implied feature of every nucleic acid sequence which encodes an amino acid. Similarly, conservative amino acid substitutions in one or a few amino acids in an amino acid sequence of a packaging or packageable construct are sequences substituted with different amino acids with highly similar properties.

It is also possible to generate other alterations in a given nucleic acid construct. Such well-known methods include site-directed mutagenesis, PCR amplification using degenerate oligonucleotides, exposure of cells containing the nucleic acid to mutagenic agents or radiation, chemical synthesis of a desired oligonucleotide, and other well known techniques. See Gilman and Smith, *Gene* 8:81-97, 1979; Roberts et al., *Nature* 328:731-734, 1987; Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989; Innis et al., PCR Protocols, A Guide to Methods and Applications,1990, Innis et al. (eds.), 21-27, Academic Press, Inc., San Diego, California; and Ausubel et al., in Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley-Interssciences (1987).

One of skill in the art can select a desired nucleic acid of the invention based upon the sequence provided and upon knowledge in the art regarding HIV generally. The life cycle, genomic organization (FIG. 2), developmental regulation and associated molecular biology of HIV viruses have been the focus of almost two decades of intense research. The specific effects of many mutations in the HIV genome are known. Moreover, general knowledge regarding the nature of proteins and nucleic acids allows one to select appropriate sequences with activity similar or equivalent to the nucleic acid sequences disclosed herein.

Finally, most modifications to nucleic acids are evaluated by routine screening techniques in suitable assays for the desired characteristics. For instance, changes in the immunological character of encoded polypeptides can be detected by an appropriate immunological assay. Modifications of other properties such as nucleic acid hybridization to a complementary nucleic acid, redox or thermal stability of encoded proteins, hydrophobicity, susceptibility to proteolysis, or the tendency to aggregate are all assayed according to standard techniques.

Packaging Vector Deletions

Specific examples, described below, will further illustrate the foreg ing general teachings. In these examples, a vector system consisting of lentivirus genetic elements includes (i) a transfer vector that shuttles a transgene with the potential for regulation and for high-titer encapsidation and (ii) creation of a packaging cell line that encapsidates vector RNA but not the viral RNA encoding the packaging components and thus be substantially helper virus free. These examples characterize the packaging signal to permit the design of packaging vectors that express components needed for packaging, but without encapsidating the coding RNA (that is, without producing helper virus). These examples also illustrate the effect of additional leader sequence mutations, as well as the effect of the replacement of the 3'-LTR on expression and packaging. These examples further demonstrate that the packaging vector can be functionally and structurally divided into two vectors. The first vector is unable to produce a functional envelope, while the second vector complements the envelope defect.

Materials and Methods for Packaging Vector Construction

Proviral DNA Clones

Parental biologically active provirus molecular clone pROD-1 of HIV-2 (ROD) virus was first modified to obtain the clone termed pROD-3. This clone was obtained by inserting a synthetic linker with a multiple cloning site and a stop codon in the *nef* gene at a site 69 amino acids downstream of the *nef* initiator codon, thus truncating it and providing new cloning sites. The pROD-3 clone was phenotypically equivalent to the parental pROD-1 clone (Arya and Sadaie, *J. Acquir. Immune. Defic. Syndr.* 6:1205-1211, 1993; Arya and Mohr, *J. Gen. Virol.* 75:2253-2260, 1994). For introducing mutations in the leader sequence, a 5'-EcoR1 - EcoR1 (nt 2658) fragment of pROD-3 was subcloned into a plasmid vector. The Bgl1 site (nt 502) of this subclone was used to create endonuclease Bal31 deletion mutants and an insertion of a synthetic BssH2 site, thus providing subclones with deletions downstream of the splice donor site (nt 470). The BssH site was then used to create upstream deletion mutants employing synthetic linkers with an additional Eag1 site at nt 305. The viral fragment from the selected subclones was reinserted into an appropriately modified pROD-3 clone. For molecular clones containing a puromycin resistance gene, the gene with or without a transcriptional termination (poly A) signal, was inserted at the engineered multiple cloning site in the truncated *nef* gene of pROD-3 clone. All mutant clones were confirmed by DNA sequencing.

Examples of various deletions are shown in FIG. 3. pROD(PK36) shown in FIG. 3A (SEQ ID NO 2) contains a 54 nucleotide downstream deletion; pROD(SK36) shown in FIG. 3B contains a 153 nucleotide upstream deletion (SEQ ID NO 3); pROD(SD36) shown in FIG. 3C contains both a 153 nucleotide upstream deletion and a 53 nucleotide downstream deletion (SEQ ID NO 4); pROD(CG36) shown in FIG. 3D (SEQ ID NO 5) contains both a 88 nucleotide upstream deletion and a 53 nucleotide downstream deletion; pROD(MR36) shown in FIG. 3E

(SEQ ID NO 6) contains both a 65 nucleotide upstream deletion and a 53 nucleotide downstream deletion.

pROD(SD36/EM) (SEQ ID NO 7) is identical to pROD(SD36) (SEQ ID NO 4); however, it also contains an insertion mutation in the envelope region as shown in FIG. 4A. To make this a vector with broader utility, other promotors, such as foreign internal promotors, can be used. For example, a CMV promotor can be used, such as pCM-ROD(SD36/EM) (SEQ ID NO 22) as shown in FIG. 4E. To be effective as a packaging vector, a vector which complements the envelope defect needs to be supplied. This complementing vector can include pCM-ENV(ROD) (SEQ ID NO 9) or pCM-VSV-G (Naldini et al., *Science*. 272:263-267, 1996) as shown in FIGS. 4B-D and 4E.

Similar packaging vectors can be generated using SIV using standard molecular biology methods. For example, an SIV equivalent of the HIV-2-based pROD(SD36), pSIV(SD36) (SEQ ID NO 11) is shown in FIG. 5B. This construct contains the functionally equivalent deletions upstream and downstream of the SD.

DNA transfection and antigen capture assays

For monolayers of epithelioid human embryonic kidney 293 or 293T cells (293 cells stably transformed with the T antigen) which were used interchangeably, 0.5-1.0 x 10^6 cells were transfected with 8-12 μg of proviral DNA using calcium phosphate transfection (see EXAMPLE 9 and Arya, *AIDS Res. Hum. Retroviruses* 9:839-848, 1993; Sadaie et al., *J. Med. Virol.* 54:118-128, 1998) and cells and culture supernatants were harvested 3 days later. Similar methods were used to transfect cell lines from several different origins (see EXAMPLE 10).

For suspension culture of human lymphoid CEM cells, 4-8 x 10^6 cells were transfected with 4-8 μg of proviral DNA by the DEAE-dextran protocol (Arya, *New Bio.* 2:57-65, 1990; Arya and Sethi, *AIDS Res. Hum. Retroviruses*. 6:649-658, 1990) and cells and culture supernatants harvested five days later. The CEM cultures were visually examined for syncytia formation before harvests. Virus particles in the supernatant were estimated by the standard antigen capture assay scoring for the p27 core protein (see EXAMPLES 1 and 2; Arya and Gallo, *Proc. Natl. Acad. Sci., USA* 93:4486-4491, 1996; Al-Harthi et al., *AIDS Res. Hum. Retroviruses* 14:59-64, 1998).

Infectivity assays

To determine the infectivity of the progeny virus, aliquots of cell-free culture supernatants from transfected cultures were incubated with CEM cells for 2-4 hours, washed twice with PBS and once with complete culture medium, and incubated for five days. Cultures were visually examined for syncytia formation and supernatant harvested for analysis. Secondary virus production was evaluated by p27 core antigen capture assays (see EXAMPLES 1 and 2).

RNA analysis

Cellular RNA was extracted by lysing cells with RNAzole (Tel-Test, Friendswood, TX) and RNA precipitated with isopropanol. The precipitate was dissolved, extracted with phenol-chloroform and re-ethanol precipitated. The precipitate was redissolved, treated with RNase-free DNase, extracted with phenol-chloroform and ethanol precipitated. For virus particle-associated RNA, clarified culture supernatant was pelleted through a column of 20% glycerol in TNE (10 mM Tris-HCl, pH 7.0; 0.15 M NaCl; 1 mM EDTA) by high speed centrifugation (Beckman SW41 rotor at 33,000 rpm for 1 hour). The pellet was lysed with RNAzole and viral RNA extracted and DNase-treated as described above.

The abundance of viral RNA was estimated by slot-blot hybridization (see for example, EXAMPLE 5). Aliquots of cellular RNA (usually, 10 - 20 μg) or viral RNA (usually half the initial amount) were denatured by heating RNA in 12 x SSC - 12% formaldehyde at 65°C for 5 minutes followed by quick cooling. Denatured RNAs were further diluted with 15 x SSC and two dilutions (1:1 and 1:5) were slot-blotted onto nitrocellulose membranes and hybridized with [^{32}P] labeled virus probe. Virus-specific RNA was quantitated by integrating the intensity of the bands with a Phosphor-Imager (Molecular Dynamics, Sunnyvale, CA) and intensity expressed in arbitrary units.

Transfer Vector Deletions

The encapsidation of the transgene in the lentiviral vector, such as HIV-1 or HIV-2, is determined by the leader sequence based bipartite packaging signal. This encapsidation is thought to be enhanced by the *gag* sequence, provided the negative effect of the *gag* inhibitory sequence is overcome by the transregulatory RRE-Rev axis. Embedded in the packaging signal is a major splice donor site that the following examples show is not by itself essential for transgene encapsidation. Redesign of the transgene vector to contain a modified splice donor site, and the upstream and downstream packaging signal, resulted in efficient transgene encapsidation by an HIV-2 packaging vector. The modified transgene vector was also encapsidated by an HIV-1 vector pseudotyped with VSV-G protein. This modification did not adversely affect transgene expression.

The packaging signal of HIV-1 and HIV-2 is multipartite with sub-elements located upstream (exonic) and downstream (intronic) of the splice donor site in the leader sequence. Inclusion of the 5' end of the *gag* gene is thought to enhance RNA encapsidation (Luban and Goff, *J. Virol.* 68:3784-3793, 1994; Miller, <u>Retroviruses</u> 437-473, 1997; Parolin et al., *J. Virol.* 68:3888-3895, 1994; Schwartz et al., *J. Virol.* 66:151-159, 1992). However, the *gag* of HIV-1 contains inhibitory/instability or cis-acting repressive (INS/CRS) sequences. These sequences downregulate expression post-transcriptionally, in part by causing nuclear retention of the transcripts and promoting their splicing and/or degradation. This negative effect on expression can

be overcome by providing RRE in cis and Rev in trans. EXAMPLES 5-9 and 17 report the unexpected finding that the splice donor of HIV-2 located in the leader sequence can use cryptic splice acceptors downstream in the vector to obtain high titer vector virus with lentiviral vectors.

Functionally equivalent transfer vectors can be generated with SIV using standard molecular biology methods. For example, an SIV equivalent of the HIV-2-based pSGT5(SDM/RRE1) (SEQ ID NO 14), pSIV(SDM) is shown in FIG. 5C (SEQ ID NO 12). pSIV(SDM) contains the functionally equivalent mutation in the SD as generated in pSGT5(SDM/RRE1).

Materials And Methods for Transfer Vector Construction

Molecular Cloning

Basic vector (clone pSGT-1) was created by deleting the central portion (nt 505 to nt 8766) of a biologically active proviral clone of HIV-2(ST) (Genbank Accesion No. M31113; Arya, *J AIDS Res. Hum. Retroviruses*. 9:839-848, 1993; Arya et al., *Human Gene Ther*. 9:1371-1380, 1998; Kumar et al., *J. Virol*. 64:890-901, 1990) and insertion of a synthetic linker to reconstitute the leader sequence up to the *gag* ATG at nt 548 (clone pSGT-2). As shown in FIGS. 6A and 6B, this clone was used to create clones pSGT-3, pSGT-4, pSGT-5 and pSGT-6, which respectively contain an insertion of the first 50, 100, 400 and 1000 nucleotides of the *gag* along with a synthetic stop placed in frame immediately after the *gag* ATG initiation codon. To these clones, a synthetic linker (SL) with multiple cloning sites was added downstream of the *gag* sequence to obtain corresponding clones termed pSGT-X(SL).

As also shown in FIGS. 6A and 6B, a cassette of a picornavirus independent ribosomal entry site (IRES) linked to the marker *neo* gene (SEQ ID NO 15) was then inserted to create clones pSGT-X(RN) (FIG. 6A), which were further modified by the addition of a 300-nucleotide fragment of HIV-2(ST) RRE1 (SEQ ID NO 19; nucleotides 7661-7960 of Genbank Accession No. M31113) (FIG. 6B) (Dillon et al., *J. Virol*. 64:4428-4437, 1990) to create clones pSGT-X(RRE1/RN). RRE1 is also referred to herein as RR or RRE. Clone pSGT-5(SDM/RRE1/RN) (SEQ ID NO 14 with the *neo* gene inserted into the multiple coning site between nt 1835-1870), abbreviated as pSGT-5(SDM), was a substitution mutant of clone pSGT-5(RRE1) (SEQ ID NO 20 with the *neo* gene inserted into the multiple coning site between nt 1835-1870) where the splice donor site was mutated from GAAGTA (nt 1023-1028 of SEQ ID NO 20) to GATATC (nt 1023-1028 of SEQ ID NO 14) to make it diverge from the consensus (see FIGS. 7A-7F). The corresponding clones containing chemokine genes were similarly created by inserting the open reading frames and associated sequences of RANTES (C-C chemokine) or SDF-1 (C-X-C chemokine) cDNA clones. Clone pSGT-5(SDX/RRE1) (FIG. 7G) (SEQ ID NO 18) is identical to pSGT-5(SDM/RRE1/RN) except that the SD mutation is a deletion mutant instead of a substitution mutant. This clone can be created using standard cloning methods.

The wild type HIV-2 (ROD) proviral clone (pROD or pROD-3) and its truncated version pROD(SD36) has been previously described herein. Clone pROD(SD36) (SEQ ID NO 4) is a deletion mutant of clone pROD-3 where the subelements of the packaging signal located upstream and downstream of the splice donor have been deleted but the splice donor site itself is preserved. The HIV-1 and VSV-G vectors (Naldini et al., *Science.* 272:263-267, 1996; Zufferey et al., *Nature Biotech.* 15:871-875, 1997) were provided by the Salk Institute.

DNA mediated transfection

Cells, for example 293T cells and those shown in EXAMPLE 10, were transfected using calcium phosphate (see EXAMPLE 9 and Arya and Gallo, *Proc. Natl. Acad. Sci., USA* 93:4486-4491, 1996; Arya and Mohr, *J. Gen. Virol.* 75:2253-2260, 1994). Typically, 1×10^6 cells from a subconfluent monolayer culture were transfected with 10 μg of vector DNA and 5-10 μg of cotransfecting DNA. Cultures were incubated with calcium-DNA aggregates overnight. Cells and culture supernatant were harvested at three days after transfection.

Protein and RNA analysis

Transgene expression was measured as described in the Examples below. For example, *neo* gene expression in transfected cells was evaluated by ELISA assays. Cellular extracts were prepared, their protein content determined, and aliquots used to measure neomycin phosphotransferase activity with biotinylated neomycin phosphotransferase antibody and avidin-horseradish peroxidase conjugate (Sadie et al., *J. Med. Virol.* 54:118-128, 1998).

For cellular RNA analysis, transfected cells were lysed with the Trizol reagent (Life Biotechnologies, Gaithersburg, MD) and RNA recovered by isopropanol precipitation. RNA was further purified by extraction with phenol-chloroform and re-ethanol precipitated. It was then digested with DNase in excess and re-extracted and ethanol precipitated. Cytoplasmic RNA was isolated by lysing cells in a hypotonic buffer and Trizol extraction. Recovery of RNA was quantitated by absorbance measurements. Viral RNA was prepared from partially purified virus particles which were pelleted through a column of 20% (v/v) glycerol by high speed centrifugation. The pellet was lysed with the Trizol reagent and viral RNA extracted and DNase treated as described above.

Abundance of vector RNA was estimated by slot-blot hybridization. Aliquots of cellular RNA (usually, 20 µg based on absorbance) or viral RNA (usually, half the amount of the total virus preparation) were denatured and two dilutions (1:1 and 1:5) were slot-blotted and hybridized with [^{32}P] labeled *neo* probe. For Northern blot analysis, about 20 µg of cellular RNA was electrophoresed in denaturing formamide-agarose gels. It was transferred to a nylon membrane by electroblotting and blot-hybridized with *neo* (or chemokine) probe. Abundance of RNA was quantitated by integrating the intensity of the bands with a Phosphor-Imager (Molecular dynamics,

Sunnyvale, CA). Where applicable, membrane was subsequently probed with a virus specific probe. Filters containing cellular RNA were also sometimes reprobed with β-actin probe. Most results reported here represent multiple independent transfections done with cells at different passages.

EXAMPLE 1

Expression of Packaging Vectors in Human Epithelioid 293 cells

Using the techniques described in the Materials and Methods for Packaging Vector Construction section above, two human cell lines, one epithelioid (293) and the other lymphoid (CEM), were tested. The cell lines were transfected with the molecular clones, and intracellular viral RNA and protein synthesis was measured to evaluate gene expression. To estimate helper virus production, extracellular release of particles containing viral RNA and proteins and their transmissibility was determined.

Expression

Figure 8 shows the measurement of intracellular viral RNA (cRNA) and protein expression (cp27) in cells transfected with the wild type and mutant HIV-2(ROD) clones containing deletions in the 5'-leader sequence.

Samples of RNA were slot-blotted onto a nitrocellulose membrane and hybridized with [^{32}P]labeled HIV-2 specific probe. Hybridization signals reflecting viral RNA abundance were quantitated using a Phosphor-Image analyzer (Molecular Dynamics, Sunnyvale, CA). The p27 levels were measured by an antigen capture (ELISA) assay. The intracellular levels of HIV-2 p27 antigen and RNA synthesized by mutant clones are expressed relative to the wild type clone. The p27 antigen level observed for wild type clone ranged from 30 to 50 ng/ml corresponding to about 0.1-0.5 x 10^6 cells. In some cases the relative abundance of intracellular viral RNA was further confirmed by Northern blot hybridization and the results were similar to those obtained by slot-blot hybridization.

Expression of the mutant clone with a short deletion of 22 nucleotides (nt 499 - 520) located downstream of the major splice donor site at nt 470 and upstream of the *gag* ATG at nt 546 (clone PK2) was not much different than the expression of the wild type clone WT. No difference was observed either for viral RNA or viral protein synthesis (where protein synthesis was measured by the estimation of the p27 core antigen in the cellular extracts). Extension of the deletion to 54 nucleotides (nt 486 - 539) in this downstream region also did not affect the expression of vector RNA and proteins (clone PK36, FIG. 3A, SEQ ID NO 2). Similar results were obtained for the mutant clone with deletion (nt 306-458) upstream of the splice donor site (clone SK36, FIG. 3B, SEQ ID NO 3).

Figure 8 shows that a deletion in the downstream region of HIV-2(ROD) of the size similar to that of the clone PK36, but extending into the splice donor site (clone PK8), had a detrimental effect on virus expression. Little or no viral RNA was detected in cells transfected with this clone. This is evidence for the importance of splicing in viral RNA processing and expression, and hence in its replication.

The clone containing deletions both downstream (nt 486-538) and upstream (nt 306-458) of the splice donor site in the leader sequence (clone SD36 in FIG. 8, also see FIG. 3C and SEQ ID NO 4) displayed diminished RNA expression relative to the wild type provirus (about one-half to one-third). This decrease was not exactly paralleled by the decline in intracellular core antigen accumulation. This can be related to the differences in the relative rates of synthesis and of half-lives of viral RNA and proteins.

The 3'-LTR provides signals for virus replication in addition to those for transcriptional termination. Thus, to minimize helper virus production, the 3'-LTR was replaced with a heterologous poly(A) signal sequence. Also, a drug resistance marker gene was included for cell selection (see SEQ ID NO 32). Thus, the 3'-LTR of selected clones was substituted with a puromycin-poly(A) cassette. Analysis showed that both the wild type and double deletion mutant could tolerate this substitution without a marked adverse effect on RNA expression relative to the parental unsubstituted clone. Similarly, the insertion of the puromycin gene at the *nef* site of the clone with an intact 3'-LTR was not detrimental for RNA expression.

In particular embodiments, it is desired that the deletion mutants decrease intracellular RNA expression by no more than 80%, and decrease intracellular p27 expression by no more than 20%.

Packaging

The effect of the same deletions and substitutions of the provirus on RNA encapsidation was measured. FIG. 9 shows a graph of the data for relative levels of viral RNA and core antigen in virus particles, which have not been normalized with respect to either the level of the intracellular viral RNA or the extracellular virus particles.

Cells were transfected with the DNA, culture supernatants were collected, an aliquot was used for p27 antigen determination, and the remaining supernatant was used for isolation of particle-associated viral RNA. Virus particles in the supernatants were collected by centrifugation through a column of glycerol. The pellets were lysed with RNAzole and RNA purified, including digestion with DNase. RNA was slot-blotted, hybridized with [^{32}P]labeled HIV-2 specific probe and quantitated. The data for mutant clones are expressed relative to the wild type clone. The level of supernatant p27 antigen ranged from 10 to 50 ng/ml. The amount of particle-associated RNA relative to that present in the cell for the wild type clone was roughly estimated to be 10% of the wild type.

The smaller deletion downstream of the splice donor site (clone PK2) did not affect virus particle production nor did it significantly affect RNA encapsidation. The larger deletion in this region (clone PK36, SEQ ID NO 2) reduced RNA encapsidation without significantly affecting virus particle production. The deletion of the upstream region (clone SK36, SEQ ID NO 3) seems to have a slightly greater effect on RNA encapsidation than the downstream deletion (clone PK36, SEQ ID NO 2). The deletion encompassing the splice donor site (clone PK8) reduced both virus particle production and viral RNA encapsidation. This was expected as this clone did not generate appreciable steady state levels of vector RNA inside the cell (FIG. 8). The clone with deletion of the leader sequence region both upstream and downstream (clone SD36, SEQ ID NO 4) displayed lowered virus particle production, but this reduction was only 30-50% of the wild type. In contrast, this clone was severely attenuated in its ability to encapsidate viral RNA, with a reduction of more than 80%, for example 90-95%.

Replacement of the 3'-LTR of this clone with the puromycin-poly(A) cassette did not further change its phenotype, it continued to produce appreciable levels of virus particles (greater than 40 or 50% of wild type) that were deficient in viral RNA (for example, less than 10% of wild type). Replacement of the 3'-LTR of the wild type clone with the puromycin poly(A) cassette (clone PA) resulted in about 50% reduction in the observed viral RNA encapsidation. A smaller degree of reduction in RNA encapsidation was also observed for the insertion of puromycin gene alone in the wild type provirus (clone PUR).

Helper virus production

To evaluate the presence of replication competent virus particles in supernatants of transfected cultures, the supernatants were used to infect CD4$^+$ CEM cells as targets and cultures monitored visually for syncytia formation and for progeny p27 core production (Table 1).

TABLE 1: Infectivity in CEM cells of progeny virus produced by Transfected 293 cells

Clone	Syncytia Induction	Progeny p27
pROD-3(WT)	+++	1.0
(PK2)	+++	1.0 ± 0.0
(PK36)	+++	0.6 ± 0.2
(PK8)	(-)	0.01
(SK36)	+	0.15 ± 0.05
(SD36)		0.01
pROD-3(PA)	+	0.03 ± 0.02
(SD36/PA)		0.01
pROD-3(PUR)	++	0.2
pSP64/pPUR	(-)	(-)

The supernatants from cultures transfected with clones PK2 and PK36 (SEQ ID NO 2) contained replication competent, syncytia inducing virus particles approaching the levels of cultures transfected with the wild type clone. The supernatants from clone SK36 (SEQ ID NO 3)

transfected cultures were also positive for syncytia induction. Thus, neither upstream nor downstream deletion alone resulted in helper virus free phenotype. In contrast, supernatants from cultures transfected with clone SD36 were essentially negative for replication competent virus particles. However, the cultures secondarily infected with this supernatant sometimes presented evidence for visually observable but minimal syncytia formation. Syncytia formation was likely due to the infecting virus or to envelope protein, but not due to the production of infectious progeny virus. The phenotype of the particles contained in the supernatant of clone SD36/PA transfected cultures was similar to those from clone SD36 transfected cultures with rare, if any, syncytia induction. The insertion of the puromycin gene into the wild type (clone PUR) appeared to attenuate its ability to produce infectious transmissible virus particles. While RNA encapsidation phenotype of the clone PUR was about 70% of the wild type clone (FIG. 9), the transmissible infectivity of the particles produced by this clone appeared to be no more than about 20% of the wild type.

EXAMPLE 2

Expression of Packaging Vectors in Human Lymphoid CEM cells

The effect of the leader sequence deletions was also determined as in EXAMPLE 1, but using human lymphoid CEM cells instead of 293 cells.

Expression

Cells were transfected with ROD leader sequence deletion mutant DNA using DEAE-dextran. Five days later, cultures were examined for the presence of syncytia and these were visually estimated in cultures transfected with mutant relative to those in cultures transfected with the wild type clone. Cells were harvested and processed for RNA isolation by the RNAzole procedure, including DNase digestion, and the abundance of virus-specific RNA determined by slot-blot hybridization.

As shown in FIG. 10, the viral RNA expression and syncytia induction phenotype of mutant clone PK2 and PK36 (SEQ ID NO 2), with deletions downstream of the splice donor site, was only modestly different from that of the wild type clone in CEM cells. In some experiments, these mutant clones synthesized viral RNA which exceeded by 20-40% the level of viral RNA synthesized by the wild type clone. Clone PK8 with deletion of the splice donor site was inactive both transcriptionally and in syncytia induction. Clone SD36 (SEQ ID NO 4)with deletions both upstream and downstream of the splice donor site was severely attenuated in viral RNA synthesis but appeared not to be as severely attenuated in syncytium induction. The fact that this clone induced observable syncytia despite reduction in viral RNA abundance suggests that syncytium induction is not directly proportional to viral RNA synthesis. Substitution of the 3'-LTR with the puromycin-poly(A) cassette can have further attenuated the phenotype of this clone as clone

SD36/PA was even less effective in syncytia induction than clone SD36. Insertion of the puromycin gene in the 3'-region at the *nef* site was also detrimental for the ability of the clone to synthesize or accumulate viral RNA and induce syncytium.

Packaging

Cells were transfected and extracellular particle-associated viral RNA (vRNA) and p27 antigen (vp27) was analyzed. The results for mutant clones are expressed relative to the wild type clone. The level of the supernatant p27 for the wild type clone was about 10 to 40 ng/ml. The estimated level of packaging of viral RNA relative to the intracellular viral RNA for the wild type clone was about 10%, a level similar to that observed with 293 cells.

As shown in FIG. 11, while the deletion of the downstream region (clones PK2 and PK36) did not remarkably affect virus particle production, it had a noticeable effect on viral RNA packaging (Table 2).

TABLE 2: Infectivity in CEM cells of progeny virus produced by Transfected CEM cells

Clone	Syncytia Induction	Progeny p27
pROD-3(WT)	+++	1.0
(PK2)	+++	0.4 0.2
(PK36)	+++	0.2 0.1
(PK8)	(-)	0.01
(SD36)	(-)	0.03
pROD-3(PA)	(-)	0.7
(SD36/PA)	(-)	0.01
pROD-3(PUR)	ND	ND
pSP64/pPUR	(-)	(-)

For example, clone PK36 (SEQ ID NO 2) produced particles whose over-all viral RNA content was about one-third of those produced by the wild type provirus clones, suggesting that the mutant was producing more empty or RNA-deficient particles than the wild type clone. As expected, a mutant clone with the deletion of the splice donor site (clone PK8) neither produced particles nor encapsidated viral RNA. Mutant clone SD36 (SEQ ID NO 4) , with deletions upstream and downstream of the splice donor site, also did not produce virus particles or encapsidate viral RNA. Replacement of 3'-LTR with puromycin-poly(A) cassette (clone PA) had a marked detrimental effect on virus production and viral RNA encapsidation. Though this clone produced detectable level of virus particles, their RNA content was too low to be reliably measured by the assay used, which was not based on the PCR-amplification of the RNA. The clone with the upstream and downstream deletion as the well as replacement of the 3'-LTR with the puromycin-poly(A) cassette (clone SD36/PA) was essentially negative in its ability to produce viral particles or RNA. The insertion of the puromycin gene in the 3'-region of the wild type clone at the *nef* site (clone PUR) appeared to attenuate viral particle production. The phenotype of this provirus in CEM cells was not extensively investigated.

In summary, a specific deletion within the downstream elements but at a distance from the splice donor site did not significantly affect the expression of viral RNA or proteins either in human epithelioid or lymphoid cells. However, these downstream deletions did affect packaging, the magnitude of effect depended on the extent of deletion, with the larger deletion causing 40 to 80% defect in encapsidation relative to the wild type. Nonetheless, these mutant proviruses with the downstream deletions continued to produce unacceptable level of infectious virus particles. The fact that CEM cultures transfected with these mutants had a lower helper virus titer than transfected 293 cultures can be related to the amplification of the primary defect by further transmission of the wild-type but not the mutant clone, in $CD4^+$ CEM but not in $CD4^-$ 293 cells. Similarly, a deletion located exclusively upstream of the splice donor site had a detrimental effect on encapsidation (60-80% reduction) but was not helper virus free in its phenotype. Thus, sequence elements located both upstream and downstream of the splice donor site in the leader sequence contribute to RNA encapsidation, and neither one can be ignored in designing helper virus free packaging vectors and transfer vectors.

The effect of the combined upstream and downstream deletion on expression was more marked and appeared to depend on the cell type. In 293 cells, the combined deletions did not significantly affect the level of viral proteins, but caused a readily observed reduction in the steady-state level of viral RNA. The reason for the discrepancy is not clear, however, the combined deletions had the desired effect on packaging. Though the deletion was accompanied by some loss of virus particle production (up to 50% relative to the wild type), the particle thus produced contained little, if any, viral RNA. Hence, this mutant provirus produced RNA deficient helper virus particles with little or no infectivity. In contrast to 293 cells, the combined deletion was accompanied by an apparent attenuation of expression and consequently also of packaging in CEM cells. This could be due to poor transfection efficiency of the CEM cells and lack of amplification of mutant as compared to wild type clone. However, the CEM cells could be transduced along with a drug resistance selection gene, and selected from drug resistance. This technique will select cells that are also enriched for expression.

Notably, deletion of the splice donor site itself resulted in the dramatic reduction in the expression of viral RNA, independent of the cell type. The observation is consistent with the idea that RNA species destined for splicing, if not spliced, are degraded and not just restricted to the nuclear compartment (Schwartz et al., *J. Virol.* 66:150-159, 1992; Malim and Cullen, *Mol. Cell. Biol.* 13:6180-6189, 1993).

EXAMPLE 3

Heter l g us Transcriptional Termination Signal

To ensure that a packaging vector could be designed that was helper-virus free but maintained the capacity to express viral genes needed for *in trans* packaging, the requirement of

the 3'-LTR for second strand synthesis, reverse transcription and virus transmission was exploited (FIGS. 8 and 9). Thus, the double deletion mutant provirus was further modified by the replacement of its 3'-LTR with a heterologous transcriptional termination signal. A puromycin resistance gene for eventual drug selection of the transduced cells was also included. This modification, pSP64/pPur, did not affect the expression capability of the vector, but further curtailed helper virus production. The replacement of the 3'-LTR with the puromycin-poly(A) cassette in wild type provirus, pROD-3(pur) was accompanied by a noticeable decline in viral RNA encapsidation.

EXAMPLE 4

Identification of Packaging Signal Sequences which are Necessary and Sufficient

To further define the sequences upstream and downstream of the SD that are necessary for packaging, other packaging vectors can be constructed. To identify the minimal amount of packaging sequence upstream from the SD that needs to be deleted to generate a functional packaging vector, vectors containing different lengths of upstream sequences can be generated. Shown in FIGS. 3D and 3E, pROD(CG36) (SEQ ID NO 5) and pROD(MR36) (SEQ ID NO 6) are packaging sequences which can be generated using standard cloning methods, which would help identify which sequences are necessary and sufficient for packaging. These two vectors contain more of the upstream SD sequences than pROD(SD36) (SEQ ID NO 4), while the downstream sequences are identical to pROD(SD36). Similar deletions can also be made downstream of the SD to identify the nucleotides necessary and sufficient for packaging. Furthermore, combinations of upstream and downstream deletions can be generated. The ability of these new packaging vectors to be expressed and packaged, for example in 293 , CEM, or other cell line, is then tested as described in EXAMPLES 1 and 2. Clones containing the maximum number of nucleotides upstream and dowstream of the SD, which express viral RNA but curtail RNA encapsidation and helper virus production, contain the minimal nucleotide deletions necessary for a functional packaging vector.

EXAMPLE 5

Expression of Transfer Vectors in Human Cells

Constitutive Expression

Human lymphocytic SupT cells were transfected with transfer vector clones (FIGS. 6A and 6B) and cellular extracts prepared to determine protein expression of the transgene neomycin (neo). Transfected cultures synthesized low but detectable levels of neo protein and RNA (data not shown). In addition, there was no marked difference in neo protein r RNA synthesis in cultures transfected with different vector clones.

The ability of the vector clones to program Neo protein and RNA synthesis in stably transfected cultures was also examined. The vectors were introduced into human lymphocytic

SupT cells and selected for G418 (*neo*) resistance for several generations. Analysis of cells transduced with different vector clones again showed that they synthesized roughly equivalent amounts of Neo protein and Neo RNA (data not shown).

Induced expression

The expression of Neo protein and RNA directed by the vector clones in the presence of transactivation provided by the HIV-2 provirus was also examined. For these studies, the replication competent HIV-2 provirus pROD-3, with functional regulatory and accessory genes (including *rev*) were used. The vector clones and provirus were co-transfected into 293T cells. Cotransfected cultures synthesized abundant quantities of Neo protein and Neo RNA (data not shown). The level of Neo protein and Neo RNA synthesized by vector clones was higher in the presence than in the absence of co-transfected provirus. This was expected as the provirus in co-transfected cultures will transactivate vector expression. The level of Neo protein and Neo RNA synthesized by different vector clones did not differ from each other significantly.

Transiently Transfected Cells

To determine if vector RNA in co-transfected cultures was encapsidated, virus particles in supernatant were partially purified and particle-associated RNA slot-blot hybridized with *neo* probe. Human epitheloid 293T cells were co-transfected with the vector and the wild-type HIV-2 proviral clone. Culture supernatants were harvested three days later and virus particles were partially purified by glycerol gradient centrifugation. Particle-associated RNA was analyzed for Neo RNA and viral RNA by slot blot hybridization with specific probes and for the content of viral p27 antigen using an antigen capture (Neo protein) assay.

As shown in Table 3, only a small fraction (less than 1%) of the Neo RNA in the cell was apparently packaged, and this did not differ among different vector clones. Similarly, all cultures encapsidated roughly equivalent amounts of viral RNA. Similar results were obtained when SupT1 cells stably transfected with vector clones were infected with HIV-2 virus. While the abundance of intracellular Neo RNA was increased relative to the uninfected cultures, only a marginal amount of Neo RNA was packaged into particles (not shown).

TABLE 3: Encapsidation of vector RNA in Human 293T Cells

	Constitutive Expression			Induced Expression and Encapsidation			
	Neo Protein		Neo RNA	Neo Protein		Neo RNA expression	Neo RNA encapsidation
	ng/ml	Relative*	Relative*	ng/ml	Relative*	Relative*	Relative*
pSGT-3 (RN)	1.8	1.0	1.0	45.0	1.0	1.0	1.0
pSGT-5 (RN)	3.4	1.9	2.1	41.8	0.9	0.8 ± 0.2	0.5 ± 0.1
pSGT-3 (RRE1)	2.9	1.6	0.6	36.5	0.8	1.0 ± 0.2	1.0 ± 0.5
pSGT-5 (RRE1)	3.8	2.1	2.2	42.0	0.9	0.8 ± 0.4	0.9 ± 0.2
pSGT-3 (SL)	0.08	<0.1	<0.1	1.0	<0.1	<0.1	<0.1

*Values are relative abundance levels.

The *neo* specific RNA in transfected culture was further characterized by Northern blot hybridization (FIG. 12). Human 293T cells were co-transfected with the wild type HIV-2 provirus pROD as well as with the leader sequence mutant provirus pROD(SD36), which synthesizes viral proteins but produces RNA-deficient particles. Cellular RNA was subjected to denaturing gel electrophoresis, electroblotted and hybridized with *neo* or RANTES probe. Northern blot analysis of RNA from transfected cultures detected two predominant RNA species hybridizing with *neo* probe for all vector clones, except for clone pSGT-5(SDM) (see below). The RNA from cultures transfected with vector clone pSGT-3(RN) contained an RNA species of about 2.9 Kb and a second species of about 2.0 Kb. Similarly, RNA from cultures transfected with other clones, except clone pSGT-5(SDM), contained two RNA species. These were about 3.2 Kb and 2.0 Kb for pSGT-5(RN) and for pSGT-3(RRE), and about 3.5 Kb and 2.0 Kb for pSGT-5(RRE).

The size of the higher molecular weight RNA species for all vector clones was consistent with the size expected from the length of the transcriptional unit contained in them. The abundance of 2.0 Kb species was always higher (3-8 fold) than that of the higher molecular species. Sometimes a third species of intermediate size was also observed but its presence and abundance was not reproducible. When the blots were rehybridized with viral and β-actin probes, all lanes showed similar bands of equivalent intensities. The observation of two different size RNA species was not unique to vector containing *neo* transgene. Two species of RNA were also observed for vector carrying C-C chemokine RANTES gene (FIG. 12) or C-X-C chemokine SDF-1 gene (not shown).

Splice donor mutant vector

A second generation derivative of the vector clone pSGT-5(RRE1/RN) (SEQ ID NO 20 the *neo* gene inserted into the multiple coning site between nt 1835-1870) was created in which the splice donor site was mutated to render it nonfunctional, clone pSGT-5(SDM/RRE1/RN), (see

FIG.6B and 7A and SEQ ID NO 14 with the *neo* gene inserted into the multiple coning site between nt 1835-1870). This clone was transfected into 293T cells in the presence of the wild type HIV-2 provirus clone pROD-3, the mutant provirus clone pROD(SD36) (SEQ ID NO 4) defective in RNA packaging and a combination of HIV-1(env⁻) and VSV-G clones. Cells were analyzed three days later for cellular *neo* and viral gene expression by slot-blot hybridization with a *neo* or virus-specific probe. As shown in Table 4, compared with the parental clone pSGT-5(RRE1/RN), mutation of the splice donor, pSGT-5(SDM/RRE1/RN), did not significantly affect the ability of the vector to direct the synthesis of Neo protein or Neo RNA. However, the splice-donor mutant vector pSGT-5(SDM/RRE1/RN) enhanced encapsidation when transfected with pROD(SD36).

TABLE 4: Enhanced encapsidation using a splice donor mutant vector

	pROD	pROD (SD36)	HIV-2/VSV-G
Neo Protein expression			
pSGT-5(RRE/RN)	115	117	135 ± 48
pSGT-5 (SDM/RRE1/RN)	133	153	121 ± 28
pSGT-5 (SL)	1	12	0.1
Neo RNA expression*			
pSGT-5(RRE/RN)	1.0	1.0	1.0
pSGT-5 (SDM/RRE1/RN)	0.8 ± 0.1	0.8 ± 0.4	0.6 ± 0
pSGT-5 (SL)	<0.1	<0.1	<0.1
Neo RNA encapsidation*			
pSGT-5(RRE/RN)	1.0	1.0	1.0
pSGT-5 (SDM/RRE1/RN)	1.9 ± 0.5	16.1 ± 4.3	2.3 ± 0.4
pSGT-5 (SL)	<0.1	<0.1	<0.1

*Values shown are relative RNA abundance levels.

The nature of the RNA synthesized by the parental and mutant clones was also analyzed by Northern blot hybridization (see FIG. 11). In contrast to the parental clone which synthesized two species of Neo RNA (about 3.5 and 2.0 Kb), the mutant clone synthesized one predominant species of about 3.5 Kb. When the supernatant particles (partially purified by glycerol gradient centrifugation) produced by the transfected culture were examined, the phenotype of the parental and mutant clone was different (Table 5).

TABLE 5 % Neo RNA Encapsidated

	HIV-2(ROD)	HIV-2 (ROD/SD36)	HIV-1/VSV-G
pSGT-5 (RRE/RN)	1.7±0.9	2.5±1.6	14.6±6.3
pSGT-5 (SDM/RRE1/RN)	4.3±2.8	24.8±11.6	30.7±5.7
pSGT-5 (SL)	<0.1	<0.1	<0.1

As shown in Table 5, in the presence of the wild type HIV-2 proviral clone HIV-2(ROD), about 2% the total transgene Neo RNA synthesized by the parental pSGT-5(RRE1/RN) clone was associated with the particles, and was about 4% for the mutant vector pSGT-5(SDM/RRE1/RN) clone. In the presence of mutant HIV-2 provirus defective for viral RNA encapsidation (pROD/SD36), the fraction of total Neo RNA in particles for the parental clone pSGT-5RRE was about 2.5%, and this fraction for the mutant clone pSGT-5(SDM) rose to about 25%. With HIV-1/VSV-G packaging vector combination, about 15% and 30% of Neo RNA synthesized by the parental and mutant clones was associated with the virus particles. These differences between the two vector clones were not related to any obvious features of the experimental protocol. Reprobing of RNA blots with virus-specific probe showed that for a given provirus, there was an equivalent amount of viral RNA on the blots. As expected, particle-associated RNA from cultures cotransfected with the mutant provirus clone pROD(SD36) contained little, if any, viral RNA. These blots were not probed with an HIV-1 viral probe. Reprobing the blots with a β-actin probe showed the slots to contain similar amounts of cellular RNA.

It has previously been reported that a part of the *gag* sequence is thought to increase encapsidation efficiency and/or selectivity. However, this region of *gag* of HIV-1, and presumably of HIV-2, had been thought to contain intragenic INS/CRS sequence elements which cause nuclear retention of the transcripts, thus curtailing their availability in the cytoplasm for packaging as well as for the expression of the attached transgene. In the past, this block has been overcome by providing RRE in cis and Rev in trans. However, in the present invention, it has been discovered that the presence of *gag* sequence in HIV-2 did not have a notable effect on expression of the attached transgene. This was irrespective of whether or not the vector contained RRE in cis and had the Rev provided in trans. Furthermore, despite the presence of leader and *gag* sequences, RNA synthesized by several vector clones was minimally packaged.

HIV-2 vector RNA was also efficiently encapsidated by the HIV-1 packaging system using VSV-G pseudotyping. There was a 2-fold difference between the parental and the splice donor mutant vector in this case. The results also demonstrate that the splice donor sequence itself is not required for packaging or transgene expression. Notably, the ability to encapsidate HIV-2 vectors in HIV-1 packaging system provides an additional margin of safety. The sequence dissimilarity between HIV-1 and HIV-2 will curtail generation of helper virus by homologous recombination during vector production. There are additional advantages of HIV-2 vectors in

comparison to HIV-1 vectors. The desirable karyophilic nuclear import function of HIV-2 is encoded by the single function Vpx. This function in HIV-1 is encoded by Vpr, which also has the undesirable cell cycle arrest function. In addition, animal models for testing HIV-2 vectors exist which may not be available for HIV-1 vectors. Also, HIV-2 is generally less pathogenic than HIV-1, thus providing better biosafety. For gene therapy of HIV-1 infection, HIV-2 vectors will be better as they are less likely to generate recombinants with the resident HIV-1 genome. Moreover, HIV-2 is believed to downregulate HIV-1.

EXAMPLE 6

Two-vector Packaging System

As described above in EXAMPLES 1 and 2, packaging vectors were generated by deleting sequences upstream and downstream of the SD site. To further minimize helper virus production, the pROD(SD36) (SEQ ID NO 4) packaging vector was split in a way that its functions were encoded by two different plasmids.

The first vector, pROD(SD36/EM) (FIG. 4A and SEQ ID NOS 7 and 21) provides all the functions except the envelope. This vector is identical to pROD(SD36) (SEQ ID NO 4), except that it contains an insertion mutation in the envelope region, rendering the envelope non-functional (see FIG. 4A). Functional equivalents can be generated by deletions, substitutions, frameshift or other mutations in this envelope region. In addition, the 5' LTR can be replaced with a foreign internal promotor (such as the CMV promotor) and 3' LTR with a heterologous polyadenylation signal (FIG. 4E and SEQ ID NO 22) to allow the vectors to be used in a wider variety of cell types.

The second vector, for example pCM-ENV(ROD) (FIG. 4B-4D and SEQ ID NO 23) or pCM-VSV-G (FIG. 4E, Naldini et al., *Science*. 272:263-267, 1996, GenBank Accession No. AF105229), compensates for the defect of pROD(SD36/EM) by providing the envelope in trans.

The ability of the three vector system to encapsidate viral RNA was compared to the two vector approach described in EXAMPLE 5. As described in EXAMPLE 5, 293T cells were transfected with the vectors as shown in Table 6. Cells were analyzed 3 days later for their ability to package viral RNA.

TABLE 6: HIV-2 Vector Packaging by Split-Genome Packaging Vectors

	% Vector RNA Encapsidated	
	HIV-2 pROD (SD36)	HIV-2 pROD (SD36/EM) + pCM-ENV (ROD)
pSGT-5 (RRE1/RN)	1.1	5.3
pSGT-5 (SDM/RRE1/RN)	9.4	29.7

As shown in Table 6, both the single packaging vector (SD36) and the two-vector packaging system [SD36/EM (SEQ ID NO 21) + pCM-ENV(ROD) (SEQ ID NO 23)] efficiently encapsidate viral RNA in the presence of the transfer vector pSGT-5 (SDM/RRE1/RN) (SEQ ID NO 14 with the *neo* gene inserted into the multiple coning site between nt 1835-1870). These results indicate that the safer-spit genome vector strategy can be used without decreasing packaging efficiency.

EXAMPLE 7

Effect of RRE Length on Transgene Expression

This example describes experiments conducted to further investigate the role of the SD site on expression of a transgene, and thus the titer attainable. In this example, the length of the RRE was varied in the transfer vector, containing the *neo* transgene (the nucleic acid sequence for *neo* is available from Genbank: nt 3596-4390 of Accession No AB003468). The identical packaging system containing pROD(SD36/EM) (SEQ ID NO 21) and the VSV-G envelope vector (pCM-VSV-G vector shown in FIG. 4E and described in EXAMPLE 6) was used to test each transfer vector.

The vector pSGT-5(RRE1/RN) (shown in FIG. 6B and SEQ ID NO 20 with the *neo* gene inserted into the multiple coning site between nt 1835-1870) which contains the *neo* gene (RN) and the wild-type splice donor (SD), was modified to contain one of two different lengths of RRE. The vector pSGT-5(RRE1/RN) (FIG. 6B) contains an RRE of 300 nucleotides (SEQ ID NO 19), while the vector pSGT-5(RRE2/RN) (SEQ ID NO 20 with the *neo* gene inserted into the multiple coning site between nt 1835-1870 and the RRE2 sequence shown in SEQ ID NO 24) contains an RRE of 530 nucleotides (SEQ ID NO 24). Using the methods described below, the level of *neo* gene expression for three different transduction vectors was measured, and the viral titer calculated for each.

Using the methods described in EXAMPLES 5 and 9, 293T cells were co-transfected with the pROD(SD36/EM) (SEQ ID NO 21) packaging vector, the VSV-G envelope vector, and serial dilutions of the lentiviral-neo vectors (see Table 7). At 48 hours post infection, cell lysates were prepared by freeze-thawing the cells in the presence of 1.0 mM PMSF (Sigma, St. Louis, MO). The protein levels were determined by assaying the crude cell lysates for Neomycin Phosphotransferase II (NPT II) using a sandwich ELISA assay. First, 96 plate microwells were coated with rabbit polyclonal antibody specific for NPT II (5Prime-3Prime, Inc., Boulder, CO) for two hours, followed by incubation with a blocking buffer (5Prime-3Prime, Inc., Boulder, CO) for 30 minutes. Dilutions of the cell lysates, standards, controls and a blank were added to individual wells and then incubated for two hours. The cells were subsequently washed and biotinylated anti-NPT II (5Prime-3Prime, Inc., Boulder, CO) was added and incubated with the cells for one hour. The wells were washed and a streptavidin alkaline phosphatase solution was added. This reaction

was incubated for 30 minutes followed by a 20-30 minute room temperature incubation with AP-substrate p-nitrophenyl phosphate for color development. The wells were then read at 405 nm using a Bio-Rad System (Bio-Rad Laboratories, Hercules, CA) against the reagent blank. From this value the number of neo-resistance colonies was determined.

As shown in Table 7, the length of the RRE had no affect on the titer obtained, and thus no affect on *neo* gene expression. However, modification of the vector to functionally delete the SD (pSGT-5(SDM/RRE1/RN); see FIG. 6B and SEQ ID NO. 14 with the *neo* gene inserted into the multiple coning site between nt 1835-1870) as described in EXAMPLE 5, enhanced the titer by approximately 30-fold. The titer shown in Table 7 is that for unconcentrated virus.

These results demonstrate that the length of the RRE has less effect on expression of the transgene, such as *neo*, than does the functional deletion of the SD site. Functional deletion of the SD enhances expression of the transgene incorporated into the transducing vector.

TABLE 7: Lentivirus-Neo Vector Transduction of Human 293T Cells

Transducing vector	Packaging vector (core)	Envelope	Titer (neo^R/ml)
pSGT-5(RRE1/RN)	pROD(SD36/EM)	VSV-G	$1.4 \pm 0.7 \times 10^4$
pSGT-5(RRE2/RN)	pROD(SD36/EM)	VSV-G	$1.6 \pm 1.0 \times 10^4$
pSGT-5(SDM/RRE1/RN)	pROD(SD36/EM)	VSV-G	$4.7 \pm 2.6 \times 10^5$

EXAMPLE 8

Expression of GFP

This example describes experiments conducted to demonstrate that other transgenes can be inserted into the lentiviral transfer vector, and be expressed. Specifically, the ability of several different transducing vectors to drive the expression of green fluorescent protein (GFP) (SEQ ID NO 25) in the presence of the pCM-ROD (SD36/EM) packaging vector (see FIG. 4E and SEQ ID NO 22) and VSV-G envelope vector (see EXAMPLE 6) was investigated.

Several different transducing vectors were constructed containing the GFP transgene (see FIG. 14 and Table 8). The transducing vectors contained either no promotor (negative control; __GFP) or GFP protein expression was driven by the CMV promotor (CM-GFP). In addition, the length of the RRE was varied as described in EXAMPLE 7 (see Table 8; RRE1, 300 nt (SEQ ID NO 19); RRE2, 530 nt (SEQ ID NO 24); and RRE3, 792 nt (SEQ ID NO 26)). The splice donor was either functionally present (SD_) or functionally deleted (SDM). The backbone transfer vector, pSGT5(SDM/RRE1/CM), (SEQ ID NO 31) which contains no transgene, was used as a negative control.

The ability of the transduction vectors shown in Table 8 in the presence f the HIV-2 packaging vector pCM-ROD(SD36/EM) (SEQ ID NO 22) and the VSV-G envelope vector to drive GFP expression in 293T cells was measured. Serial dilutions from 1/10 to 1/100,000 of lentiviral-

GFP vectors were prepared from a primary viral harvest (unconcentrated). The 293T cells were exposed to the GFP vectors for 14 - 16 hours vectors to transduce the cells as described in EXAMPLE 5.

The cells were subsequently analyzed for GFP expression 48 hours later by flow cytometry using the following method. Cells were gently washed once with PBS (phosphate buffered saline) and detached from the plate with 1 mM EDTA in PBS for 15 minutes at RT with slow shaking. The cells were resuspended by gentle pipetting then fixed in 2% para-formaldehyde for one hour on ice. After removing the para-formaldehyde, the cells were resuspended in PBS containing 2% FBS (fetal bovine serum) and GFP expression measured using cell sorting flow cytometry.

From this analysis, the viral titer was calculated in transduction units (TU) per ml (TU/ml). The viral titers shown in Table 8 are the lowest dilution of vector used to transduce the 293T cells in which GFP fluorescence is still observed. Titer values below those shown in Table 8 did not produce detectable GFP expression by the transduction vector.

As shown in Table 8, varying the length of the RRE in the leader sequence had little to no affect on viral titer, and thus on GFP transgene expression. However, the titer droped by 10-fold in the presence of a functional SD [HIV-2(SD_ /RRE1/CM-GFP)].

The results in Table 8 also demonstrate the effect of the presence or absence of a promotor to drive gene expression. The internal promoter CMV allowed expression of the GFP transgene (Table 8, all vectors containing "CM"). These results demonstrate that expression of a transgene can be achieved by using a foreign internal promotor, such as CMV, or by using a native promoter such as LTR (which was used above to drive *neo* expression; for example see Table 7 in EXAMPLE 7). However, a very low titer is observed if no promoter is present to drive expression of the transgene [HIV-2(SDM/RRE1/__GFP)]. The advantage of using internal promotors such as CMV is that CMV can function in many cells, while LTR requires viral TAT or a cellular homologue of TAT.

In conclusion, these results demonstrate that mutation of SD is important for transgene expression, irrespective of: the length of the RRE; the nature of the transgene (neo or GFP; expression of other transgenes are shown in EXAMPLES 11-14); whether the transgene is directed by the native LTR promoter or a foreign internal promoter; the presence or absence of IRES; and the presence or absence of introns.

TABLE 8: Lentivirus-GFP Vector Transduction of Human 293T Cells:

Transducing vector	Packaging vector(core)	Envelope	Titer (TU/ml)
HIV-2*(SDM/RRE1/CM-GFP)	pCM-ROD(SD36/EM)	VSV-G	$3.2 \pm 1.3 \times 10^5$
HIV-2(SDM/RRE2/CM-GFP)	pCM-ROD(SD36/EM)	VSV-G	$4.3 \pm 1.7 \times 10^5$
HIV-2(SDM/RRE3ST/CM-GFP)	pCM-ROD(SD36/EM)	VSV-G	$3.4 \pm 2.0 \times 10^5$
HIV-2(SD_ /RRE1/CM-GFP)	pCM-ROD(SD36/EM)	VSV-G	$4.2 \pm 2.0 \times 10^4$
HIV-2(SDM/RRE/__GFP)	pCM-ROD(SD36/EM)	VSV-G	$\leq 10^4$
pSGT-5(SDM/RRE1/CM)	pCM-ROD(SD36/EM)	VSV-G	<<

*HIV-2 is pSGT-5

EXAMPLE 9

Concentration of Transfer Vectors

This example describes methods used to concentrate transfer lentivirus-GFP vectors. Similar methods can be used to concentrate any of the lentivirus vectors, for example a transfer lentiviral vector containing a therapeutic transgene. Concentration of the transfer vectors results in higher viral titers.

The viral vectors were concentrated as follows. One day before transfection, cells were plated at 0.5-1.5 x 10^6 cells per 75cm T-flask in 12 ml of complete medium and incubated at 37°C, 5% CO_2. The following day, the medium was removed and eight ml of fresh medium was added and the cells incubated for 3-4 hours. Calcium-DNA precipitates were prepared as recommended by the manufacturer of the transfection kit (Life technologies, Gaithersburg, MD or Promega, Madison, WI) with the following specifications: 8-12 μg vector DNA (usually 10 μg) + 6-10 μg packaging DNA (usually 6 μg) + 4-6 μg envelope DNA (usually 4 μg). The calcium-DNA mixtures were added to cultures dropwise with gentle mixing. The cells were subsequently incubated at 37°C, 5% CO_2 for 60-68 hours. Following the incubation, the culture medium (containing the viruses) was collected into a 15 ml sterile tube, which was centrifuged at 1200 rpm for five minutes. The clarified medium was filtered through a 0.45 μm syringe filter.

To further concentrate the virus, the following procedure was used. The filtered medium was centrifuged at ~ 50,000 x g for 90 minutes at 4°C using an appropriate ultracentrifuge rotor and speed. For example, the following can be used: Beckman Type 60Ti rotor at 30 -35,000 rpm or a Beckman Type 50Ti rotor at ~35, 000 rpm. The resulting pellet was suspended in 1/200th of the starting volume (e.g., 0.8 ml for 120 ml starting volume) of cold TBS (50 mM Tris-HCl, pH 7.8; 130 mM NaCl; 10 mM KCl; 10 mM $MgCl_2$) containing 0.1 mM each of dNTP (dATP, dGTP, dTTP, dCTP), 3 mM spermine and 0.3 mM spermidine. This suspension was incubated at 37°C for two hours. Following the incubation, the suspension was diluted with enough cold TBS containing 5 mM $MgCl_2$ to fill the centrifuge tube (for example to ~12 ml for Type 50Ti rotor) and centrifuged at 50,000 x g for 90 minutes. The final pellet was suspended in 1/500th of the

volume of the original culture medium in sterile, cold PBS (phosphate buffered saline), and aliquoted into 20 μl aliquots (e.g., 15 x 20 μl for 160 ml)

The 293T cells were transfected using serial dilutions of the concentrated vectors and the titer of the concentrated viruses calculated using the methods described in EXAMPLES 5 and 7. The transfer vector used was pSGT-5 (SDM/RRE1/CM-GFP). This vector was created by inserting the GFP sequence (SEQ ID NO 25) into the MCS (Xho1 cloning site at nt 2908 downstream of the CMV promoter) of pSGT-5(SDM/RRE1/CM) (SEQ ID NO 31). The packaging vectors used were pCM-ROD (SD36/EM) (SEQ ID NO 22) and pROD(SD36/EM) (SEQ ID NO 21) as shown in FIG. 4E. The envelope vector used was pCM-VSV-G (FIG. 4E, see EXAMPLE 6).

As a positive control, the ability to concentrate HIV-1 vector was also examined using the pHR-CM-GFP transducing vector (Salk Institute) and an HIV-1(CMV) packaging vector with the pCM-VSV-G envelope vector (FIG. 4E).

As shown in Table 9, the lentivirus vector can be concentrated using ultracentrifugation, to a level of at least 4 x 10^7 TU/ml. These results demonstrate that the HIV-2 lentiviral vectors can be concentrated several hundred-fold, similar to the results achieved with the HIV-1 lentiviral vectors. As shown in the examples below, the titers obtained by ultracentrifugation are sufficient to transduce a variety of cell types.

TABLE 9: Titer of Lentivirus-GFP Vectors on Human 293T Cells

Transducing vector	Packaging vector (core)	Envelope	Uncon-centrated	Centriprep-50	Centriprep-50 + Ultracentrifuge	Ultra-centrifuge
HIV-2	pROD(SD36/EM)	VSV-G	6 x 10^4	--	--	2 x 10^6
	pCM-ROD (SD36/EM)	VSV-G	2 x 10^5	5 x 10^6	8 x 10^7	4 x 10^7
HIV-1	HIV-1 (CMV)	VSV-G	1 x 10^6	3 x 10^7	6 x 10^8	2 x 10^8
Untransduced	--	--		<0.1%		

EXAMPLE 10

Transduction of Several Human Cell Types

This example describes experiments in which the lentivirus-GFP vector HIV-2(SDM/RRE1/CM-GFP) (see EXAMPLE 9) was transduced into several different types of human cells, to demonstrate that transduction can occur in a wide variety of cell types. These methods can be used to determine the ability of other transduction vectors to transduce other cell types from different organisms. For example, the ability of a transfer lentiviral vector, such as a vector containing a transgene to be expressed in a cell in which that transgene is not endogenously

expressed at normal levels, to transduce a cell of interest, can be determined using the methods described herein.

The following cell types were tested. Most cell lines were obtained from The American Type Culture Collection (ATCC, Manassas, VA). The 293 (ATCC #CRL1573) and 293T cells were cultured in Dulbecco's Modified Eagle Medium (DMEM) with 10%Fetal Bovine Serum (FBS). HeLa cells (ATCC # CCL-2) were cultured under standard conditions. Fabry fibroblasts (OMN 94.3) and normal skin fibroblasts CD-27sk (ATCC #CRL-1475) were maintained in DMEM with 10% FBS. SVG (ATCC CRL-8621) and HFGC cells were grown in Minimal Essential Medium (MEM) with L-glutamine and 10% FBS. SVG-neural differentiated cells were cultured in Neurobasal Medium with L-glutamine, N2 supplement (neurotropic factors) and 1% FBS. SKN-MC (ATCC #HTB-10); SKN-SH; U281 and U373 (ATCC # HTB-17) cells were also tested.

Two different transfer vectors were tested: pGST-5 (SDM/RRE1/CM-GFP) (see EXAMPLE 9 and FIG. 14) and HIV-1(CMV) (Salk institute). Ultracentrifuged-concentrated transfer virus (EXAMPLE 9) was transduced into the cell lines listed in Table 10 at a multiplicity of infection (MOI) of 5.0, 1.0, 0.5, 0.1 or 0.01, using the methods described in EXAMPLES 5 and 7. The packaging vector for HIV-2 was pCM-ROD (SD36/EM) (SEQ ID NO 22) and for HIV-1 was HIV-1 (CMV). The envelope vector VSV-G was used for all experiments. The percent of cells transduced at each MOI was calculated by flow cytometric cell sorting and dividing the number of fluorescent cells by the total number of cells in the sample.

As shown in Table 10, the HIV-2 GFP vector transduced cells of several different origins as well as observed by HIV-1 GFP. This transduction resulted in expression of the GFP transgene in all cell types tested. Table 11 shows the statistical analysis for experiments using primary fetal brain cells. The advantage of the HIV-2 vector system is that it is a safer vector than HIV-1, but is still able to transduce cells as well as HIV-1. In conclusion, these results demonstrate that the lentiviral system of the present invention has the ability to express the transgenes incorporated into the transfer vector in a wide variety of cells from different origins.

TABLE 10: Lentivirus-GFP Transduction of Human Cells

Cells	Characteristic	HIV-2 GFP % Cells transduced at MOI of				HIV-1 GFP % Cells transduced at MOI of		
		1.0	0.1	0.01		1.0	0.1	0.01
293	Kidney epitheloid	33	9	--		47	13	--
HeLa	Ovarian epitheloid	52	8	--		62	15	--
CD27sk	Skin fibroblast	62	15	--		81	26	--
OMN 94.3	Fabry fibroblast	58	14	--		71	17	--
SVG	Fetal brain/SV40	56	17	1		82	28	5
SVG-differentiated	Fetal brain/SV40	50	11	2		70	29	5
HFGC	Primary fetal brain	55	20	2		69	27	4
		5.0	1.0	0.5	0.1	5.0	1.0	0.1
SKN-MC	Neuro-epithelioma	46	--	16	--	58	--	--
SKN-SH	Neuroblastoma	50	51	--	3	58	58	15
U281	Glioma	68	63	--	17	92	91	40
U373	Glioma	68	56	--	9	92	80	40

TABLE 11. Lentivirus-GFP Transduction of Primary Human Fetal Brain Cells *in vitro*

Transducing vector	Packaging vector (core)	Envelope	% Cells Transduced MOI = 1	% Cells Transduced MOI = 0.1
HIV-2	HIV-2	VSV-G	54 ± 8	9 ± 5
--	HIV-2	HIV-2	0.1	0.1
HIV-1	HIV-1	VSV-G	77 ± 9	26 ± 11
Untransduced			<0.1	<0.1

EXAMPLE 11

Fabry Disease M del

This example describes the generation and testing of therapeutic vectors that can be used to deliver genes to cells, such as cells of individuals suffering from a deficiency in α-galactosidase (α-GAL-A) expression. Cell delivery can be either *in vitro* or *in vivo*. For example, the lentiviral

vectors described herein can be used for gene therapy to treat individuals suffering from Fabry disease, an inborn error of metabolism. Individuals suffering from Fabry disease are α-GAL-A deficient, and as a result, deposit large amounts of glycolipid in their cells. By providing the *α-GAL-A* gene in trans, for example by expressing α-GAL-A in the cells of a Fabry individual using the lentiviral transducing, packaging and envelope vectors of the present invention, the cells of a Fabry individual would be expected to clear the excess cellular glycolipid.

An HIV-2 transducing vector containing the *α-gal* gene, HIV-2(CM-α-GAL-A), was constructed as shown in FIG. 14. Briefly, the murine *α-GAL-A* gene sequence (SEQ ID NO 27) was cloned into the MCS of the transfer vector pGST-5 (SDM/RRE1/CM) (SEQ ID NO 31). Alternatively, the human (or any other species)*α-GAL-A* gene sequence can be used (Genbank Accession No X14448).

Fabry fibroblasts (OMN 94.3 and 98.5) were transduced *in vitro* with concentrated lentiviral-α-GAL-A vectors shown in Table 12, using the methods described in EXAMPLES 5 and 7. As a control, both an HIV-1 (HIV-1 (CMV)) and an HIV-2 [pCM-ROD (SD36/EM) (SEQ ID NO 22)] packaging vector along with the VSV-G envelope vector were tested. Following the transduction (48 hours later), cells were detached from the plates using trypsin and washed with PBS. The cells were resuspended in homogenization buffer (28 mM citric acid, 44 mM disodium phosphate, 3 mg/ml sodium taurocholate, pH 4.4) and sonicated 5 x 10 seconds on ice. To assay for the level of α-GAL-A protein expressed, 150 μl of the substrate 5 mM 4-methylumbelliferyl-α-D-galactopyranoside (4MU) was added to the cell extracts with and without the α-galactosidase B inhibitor, N-acetyl-galactosamine. The mixture was incubated at 37°C for 30 minutes. The enzyme reaction was stopped by adding stop buffer (0.1 M glycine; 0.1 M NaOH). The fluorescent values at 336 nm were read against a water blank. A standard curve for 4MU was plotted and the specific enzyme activity was calculated as nmole/hr/mg protein. Normal individuals have an α-GAL-A activity of 130 - 370 nmoles/hr/mg while Fabry individuals have reduced α-GAL-A activity of 2 - 20 nmoles/hr/mg.

As shown in Table 12, untransduced Fabry cells have an α-GAL-A activity of between 50-118. However, upon expression of the *α-gal* gene using the lentivirus system of the present invention, levels of α-GAL-A in the Fabry fibroblasts increased dramatically. Therefore, high-levels of expression of α-GAL-A can be achieved using the lentiviral vectors of the present invention. Similar results were obtained with the HIV-1 and HIV-2 packaging vectors.

TABLE 12. Lentivirus-α-GAL-A Transduction of Human Fabry Fibroblasts *in vitro*

Transducing vector	Packaging Vector (core)	Envelope	α-GAL-A activity (nmoles/hr/mg)	
			In 98.5 cells	In 94.3 cells
HIV-2(CM-AGA)	HIV-2	VSV-G	2,730 ± 420	1,860 ± 1,700
	HIV-1	VSV-G	2,680 ± 1,720	1,350 ± 750
HIV-2(CM-AGA/Rpuro)	HIV-2	VSV-G	2,520 ± 1,990	
	HIV-1	VSV-G	4,600 ± 1,550	
Untransduced	--	--	118 ± 114	50 ± 50

To determine if the increased expression of the *α-gal* gene in Fabry fibroblasts would result in the clearance of excess cellular glycolipids, the following assay was conducted. After determining that the cells were expressing near-normal levels or higher of the *α-gal* gene, (see Table 12), the cells were analyzed using a CTH clearance assay.

Fabry fibroblasts were transduced with lentiviral-α-GAL-A vectors for 14-16 hours and 48 hours were allowed for *α-gal* gene expression. The medium was removed and the cells were washed twice with PBS. The cells were incubated overnight with DMEM containing 3 nM nM/ml of lysamine-rhodamine conjugated cerebotrihexosamide (CTH) in the absence of serum. The next day, the CTH was removed and the cells washed twice with PBS. Subsequently, the cells were incubated in DMEM containing 10% FBS. The cells were observed periodically after 6 hours, 24 hours and 48 hours using a florescence microscope at 32x, 20x and under phase contrast. A decrease in cellular florescence indicated that glycolipid was being cleared from the Fabry cells.

The results of these experiments demonstrate that Fabry fibroblasts expressing the *α-GAL-A* transgene clear glycolipids better than Fabry fibroblasts that were not transduced with the *α-GAL-A* gene. Therefore, lentiviral vectors of the present invention which allow expression of a functional *α-GAL-A* gene can be used to deliver the *α-GAL-A* gene into the cells of Fabry patients suffering from decreased *α-GAL-A* expression and from accumulation of glycolipid in their cells.

One skilled in the art will recognize that the exact full-length α-GAL-A nucleic acid sequence shown in SEQ ID NO 27 will not be the only sequence that will allow expression of functional *α-GAL-A*. For example, the amino acids can be conservatively substituted (see Definitions section) or the nucleic acid sequence can altered to encode the identical amino acid by using a different triplet encoding that amino acid. In addition, alternative species of α-GAL-A can be used.

EXAMPLE 12

Parkinson's Disease Model

This example describes the generation and testing of therapeutic vectors that can be used to deliver genes to cells, such as cells of individuals suffering from a deficiency in aromatic amino acid decarboxylase (AADC) expression. Cell delivery can be either *in vitro* or *in vivo*. For example, the lentiviral vectors described herein can be used for gene therapy to treat individuals suffering from Parkinson's disease. Individuals suffering from Parkinson's disease suffer from the loss of substantia nigra neurons, which results in depletion of the neurotransmitter dopamine in the hypothalamus. As a result, Parkinson's patients suffer from a biochemical pathway defect in their neurons, specifically the inability to convert L-dopa into L-dopamine.

One approach to treating Parkinson's disease is to convert L-dopa into L-dopamine, by expressing the aromatic amino acid decarboxylase (AADC) gene in the region of the brain where dopamine is depleted. For example, the lentiviral transducing and packaging vectors of the present invention can be used to express AADC in neural cells for gene therapy to treat individuals suffering from Parkinson's disease. By providing the *AADC* gene in trans, for example by expressing AADC in the cells of a Parkinson's patient, the neurons of a Parkinson's individual would be expected to convert L-dopa in their cells to L-dopamine.

Two HIV transfer vectors containing the *AADC* gene were constructed: HIV-1 AADC and HIV-2 AADC (see FIG. 14). The sequence of HIV-2 AADC was obtained by inserting the human *AADC* gene sequence (SEQ ID NO 28) into the cloning site of the transfer vector pGST-5 (SDM/RRE1/CM) (SEQ ID NO 31).

Each of the HIV AADC transfer vectors were individually used to transform human fetal brain cells *in vitro*, using the methods described above. As a control, both an HIV-1 (HIV-1 (CMV)) and an HIV-2 [pCM-ROD (SD36/EM) (SEQ ID NO 22)] packaging vector were used with the VSV-G envelope vector (FIG. 4E). Subsequently, the conversion of L-dopa to L-dopamine was measured as described below. Similar methods can be used to test the ability of the HIV-2 AADC vector to convert L- dopa to L-dopamine.

Cells (SVG, HFGC, and SVG-differentiated) were transduced with HIV-1-AADC. Forty-eight hours post infection, the cells were washed once with HEPES buffered saline which was left on the cells for one minute. After removing the buffered saline, 4 μM L-dopa in HEPES buffered saline was added and the samples incubated for 30 or 60 minutes with L-dopa buffer. At the end of the specified time, a 150 μl aliquot of the buffer was added to a tube containing 15 μl of lysis solution (0.1 N perchloric acid, 1% ethanol, 0.02% EDTA) and the sample stored on dry ice. To the remainder of the buffer, 1 ml of the lysis solution was added to the cells and the sample placed on dry ice. The dopamine and other metabolite levels were measured by HPLC.

As shown in Table 13, uninfected SVG and HFGC cells are unable to convert L-dopa to L-dopamine even after 60 minutes. However, expression of AADC by the HIV-1 AADC transfer

vector results in the ability of these same cells to convert L-dopa to L-dopamine. The described herein can be used to test the ability of HIV-2 AADC to express AADC and result in the ability of AADC deficient cells to convert L-dopa to L-dopamine.

One skilled in the art will recognize that the exact full-length AADC nucleic acid sequence shown in (SEQ ID NO 28) will not be the only sequence that will allow expression of functional AADC. For example, the amino acids can be conservatively substituted or the nucleic acid sequence can altered to encode the identical amino acid by using a different triplet encoding that amino acid.

TABLE 13: HIV-1 AADC Transduction of Human Fetal Brain Cells

Cells	% Conversion from L-dopa to L-dopamine	
	30 minutes	60 minutes
(a) Secreted		
SVG cells	19.0	(6.5)
SVG cells - differentiated	39.2	46.0
HFGC- primary, short term	24.5	51.0
Uninfected SVG/HFGC	0	0
(b) Intracellular		
SVG cells	72.4	59.2
SVG cells - differentiated	91.4	76.7
HFGC - primary, short term	86.5	95.0
Uninfected SVG/HFGC	0	0

EXAMPLE 13

Infectious Disease Model

This example describes the generation and testing of therapeutic lentiviral vectors that can be used to deliver genes to cells, such as cells of individuals suffering from an infectious disease. Cell delivery can be either *in vitro* or *in vivo*. For example, the lentiviral vectors described herein can be used for gene therapy to treat individuals suffering infectious diseases, such as AIDS resulting from HIV infection. Treatment of infectious diseases is be aided by achieving high local secretion of antiviral chemokines to block infection and inhibit the virus. In addition, virus inhibition can be achieved by intracellular expression of a mutant chemokine to block infection from within and achieve intracellular immunization.

Several HIV transfer vectors containing the *RANTES* gene were constructed (see FIG. 14 and Table 14). HIV-2(CM-Rant-Rpuro), HIV-2(CM-RantKD-Rpuro), and HIV-2(CM-Rant8A-Rpuro) (see Table 14) were constructed. Rant is the RANTES shown in SEQ ID NO 29. RantKD contains a SKDEL tag on the carboxy terminus and Rant 8A is a substitution mutant. These

transfer vectors were generated by inserting the RANTES sequence (or variation thereof) into the cloning site of pSGT-5(SDM/RRE1/CM) (SEQ ID NO 31).

Each of the HIV-2 RANTES transfer vectors were individually used to transform human 293T cells *in vitro*, using the methods described above. The packaging vectors used were the HIV-1 and HIV-2 packaging vectors used in EXAMPLES 9-12, with the VSV-G envelope vector (FIG. 4E)..

Supernatants and cell lysates from cells transduced with lentiviral-RANTES vectors were collected and assayed for RANTES protein concentration (the amount secreted into the media and the intracellular amount) was measured using a quantitative sandwich ELISA assay. Microwells of an ELISA plate were coated with a murine monoclonal antibody to RANTES (5Prime-3Prime, Inc., Boulder, CO). To each well, either standards, blanks, diluted supernatants or cell lysates were added and incubated for two hours. The cells were washed and horseradish peroxidase (HRP) conjugated polyclonal antibody to RANTES was added and incubated for one hour. The wells were subsequently washed and to the wells, a color substrate (tetramethylbenzidine in hydrogen peroxide) was added and incubated for 20 minutes. Sulfuric acid (2N) was added to stop the reaction. The reaction in each well was read at 450 nm against the blank.

As shown in Table 14, RANTES protein is expressed in the cells transformed with the RANTES sequence (SEQ ID NO 29). However, no detectable RANTES protein was detected in the cells transformed with the substitution mutant (Rant 8A). Higher levels of expression were observed in the cells transfected with the RantKD sequence.

In addition to RANTES, other chemokines can be used in the present invention. Similar methods can be used to test the ability of any lentiviral vector to containing a chemokine gene to express that gene product.

TABLE 14: Lentivirus-RANTES Transduction of Human 293T Cells

Transducing Vector	Packaging vector (core)	Envelope	RANTES Protein	
			Secreted (ng/ml)	Intracellular (mg/mg protein)
HIV-2(CM-Rant-Rpuro)	HIV-2	VSV-G	0.96 ± 0.16	0.25 ± 0.05
HIV-2(CM-Rant-Rpuro)	HIV-1	VSV-G	3.8 ± 0.3	5.17 ± 4.0
HIV-2(CM-RantKD-Rpuro)	HIV-2	VSV-G	2.4 ± 0.4	1.15 ± 0.45
HIV-2(CM-RantKD-Rpuro)	HIV-1	VSV-G	2.5 ± 0.2	1.9 ± 0.4
HIV-2(CM-Rant8A-Rpuro)	HIV-2	VSV-G	<<	<<
HIV-2(CM-Rant8A-Rpuro)	HIV-1	VSV-G	<<	<<
Uninfected 293 T			0.05	0.2

EXAMPLE 14

Apoptosis M del

This example describes the generation of therapeutic lentiviral vectors that can be used to deliver genes to cells, such as cells of individuals suffering from a defect in cell cycle regulation. Cell delivery can be either *in vitro* or *in vivo*. For example, the lentiviral vectors described herein can be used for gene therapy to treat individuals suffering from cancer, in which there is either an up or downregulation of apoptosis.

Genes which are known to regulate apoptosis can be inserted into the cloning site of the HIV-2 lentiviral backbone vector of the present invention (SEQ ID NO 31). Any of the genes known to regulate the cell cycle, such as BAX, can be cloned into the cloning site of SEQ ID NO 31. One such example is shown in FIG. 14.

BAX expression, or the expression of any other gene involved in regulating the cell cycle, can be monitored using standard methods, for example ELISA assays or flow cytometric methods such as those described in the above examples.

EXAMPLE 15

Testing Lentivirus Vectors *in vivo*

The lentiviral vectors described in the above examples can be tested for their ability to express a transgene in mouse models which have been generated for various diseases. Mice which are functionally deleted for a transgene, are infected with a transfer vector containing the transgene along with a packaging vector. Mice are then screened for their ability to express the transgene, and the ability of the transgene to correct the phenotypic affect of the transgene deletion.

EXAMPLE 16

Gene Therapy using Lentivirus Vectors

A new gene therapy approach for patients using the lentiviral transfer and packaging vectors taught by the present invention, is now made possible by the present invention. Essentially, cells can be removed from a subject having deletions or mutations of a gene, and then transfected with the packaging and transfer vectors (which contains the therapeutic transgene). These transfected cells will thereby produce functional transgene protein and can be reintroduced into the patient. Methods described in US Patent No. 5,162,215 (Bosselman et al.) (herein incorporated by reference) demonstrate how to detect the presence and expression of a gene of interest in target cells. Methods described in US Patent No. 5,741,486 (Pathak et al.) (herein incorporated by reference) teach the use of retroviral vectors in gene therapy. Methods described in PCT WO 98/39463 (here in incorporated by reference) demonstrates other approach to construction and use of lentivrial vectors ass a gene transfer vector. Such methods can be applied to the lentiviral vectors of the present invention, for example in gene therapy.

The scientific and medical procedures required for human cell transfection are now routine procedures. The provision herein of lentiviral transfer and packaging vectors now allows the development of human and non-human gene therapy based upon these procedures.

In some embodiments, the present invention relates to a method of treating patients which underexpress a transgene, or in which greater expression of the transgene is desired. These methods can be accomplished by introducing a gene coding for the therapeutic transgene into a transfer vector, which is subsequently introduce into the patient along with a packaging vector.

In some of the foregoing examples, it may only be necessary to introduce the genetic or protein elements into certain cells or tissues. For example, in the case of benign nevi and psoriasis, introducing them into only the skin may be sufficient. However, in some instances (i.e. tumors and polycythemia inflammatory fibrosis), it may be more therapeutically effective and simple to treat all of the patients cells, or more broadly disseminate the vector, for example by intravascular administration.

The transfer and packaging vectors can be administered to the patient by any method which allows the vectors to reach the appropriate cells. These methods include injection, infusion, deposition, implantation, or topical administration. Injections can be intradermal or subcutaneous.

EXAMPLE 17

Specificity of HIV Packaging

The ability of HIV-1 and HIV-2 to "cross-package," that is package the other species RNA, was investigated. Human 293T cells were transfected with a transfer vector and a packaging vector as shown in FIG. 13. The ability of the vectors to package its own RNA was compared to its ability to package the other HIV species as described in EXAMPLE 5.

As shown in FIG. 13, there is a 4-5 fold increase in the specificity of HIV-2 packaging compared to HIV-1. HIV-2 packages 8% of vector RNA in the presence of an HIV-2 transfer vector [pSGT-5 (SDM); SEQ ID NO 14], but only 1% in the presence of an HIV-1 transfer vector (pHR-CM-LUC). This is an 8-fold difference. In contrast, HIV-1 packages 16% of the vector RNA in the presence of an HIV-1 transfer vector, and 10% in the presence of an HIV-2 transfer vector. This is only a 1.5-2 fold difference.

The titer of vector obtained was also investigated. Using the methods described above, 293T cells were transduced with an HIV-1 [HIV-1(CMV)], or an HIV-2 [pSGT-5(SDM/RRE1/CM-GFP)] transfer vector. As shown in Table 15, the HIV-1 packaging vector can package the transgene present in both the HIV-1 and HIV-2 vector RNA, whereas the HIV-2 packaging is more specific in preferentially encapsidating its own vector RNA than HIV-1 vector RNA.

TABLE 15: Lentivirus-GFP Vector Transduction of Human 293T Cells

Transducing vector	Packaging vector (core)	Envelope	Titer (TU/ml)
HIV-2	HIV-2	VSV-G	$1.1 \pm 0.8 \times 10^5$
HIV-2	HIV-1	VSV-G	$2.0 \pm 0.8 \times 10^5$
HIV-2	HIV-2/Env-	HIV-2	$< 4.0 \times 10^4$
HIV-1	HIV-2	VSV-G	$2.2 \pm 0.6 \times 10^4$
HIV-1	HIV-1	VSV-G	$1.6 \pm 0.6 \times 10^6$
HIV-1	HIV-2/Env-	HIV-2	$< 2.0 \times 10^4$
Untransduced	--	--	--

In summary, the HIV-2 packaging is more stringent while HIV-1 packaging more promiscuous. These results indicate that HIV-2 packaging yields better quality vector and as a result also a higher titer than HIV-1 packaging. This observation can be further exploited by designing a hybrid packaging system using split genome strategy (see EXAMPLE 6) where the envelope-defective HIV-2 packaging vector will be complemented with an HIV-1 envelope expression plasmid. The RNA encoded by HIV-1 plasmid will not be co-packaged by the HIV-2 packaging vector, thus achieving another built-in safety feature.

EXAMPLE 18

SIV Packaging and Transfer Vectors

The generation of packaging (EXAMPLES 1-4, 6) and transfer (EXAMPLES 5-14) lentiviral vectors was described above. Given the similarities in the genomic organization of HIV and SIV, one skilled in the art could apply what was learned from HIV-2 to SIV. For example, an SIV packaging vector can be generated by making upstream and downstream SD deletions as described above for HIV-2. Specifically, an SIV pROD(SD36) homologue, pSIV(SD36) (FIG. 5B; SEQ ID NO 11) can be generated using standard molecular biology methods. This SIV packaging vector could also be divided into two parts, as described in EXAMPLE 6. The envelope region of pSIV(SD36) can be mutated to render it non-functional, while another vector containing the functional envelope in trans would be provided to compensate for the envelope defect.

An SIV transfer vector can be generated by generating a functional mutation in the SD site. The SIV pSGT-5 (SDM) homologue, pSIV(SDM) (FIG. 5C; SEQ ID NO 12), can be generated using standard molecular biology methods.

The ability of these vectors to function as transfer and packaging vectors could be tested by the methods described in EXAMPLES 1-5, and for the ability to express specific transgenea as described in EXAMPLES 7-14.

EXAMPLE 19

Use of the Nucleic acids of the Invention as Molecular Probes

In addition to their utility in making HIV packaging cell lines, the non-infective packaging vectors of the invention can be used to detect wild-type HIV in biological samples using Southern or northern blot assays. In brief, the packaging vector is labeled, typically using a radio or bioluminescent label, and used to probe a northern or Southern blot of a sample suspected of containing HIV virus. The use of the packaging vector as a probe is safer than the use of an infective virus as a probe. The packaging vector is also more likely to detect a wild type virus than a smaller probe because, unlike a small probe, the packaging vector probe has virtually the entire genome in common with a wild-type virus, making it improbable that the wild type virus could escape detection by mutation of the probe binding site.

Furthermore, the packaging vectors can be used as positive controls in essentially all known detection methods for the detection of HIV. In this embodiment, a packaging vector nucleic acid or encoded polypeptide is used as a positive control to establish that an HIV detection assay is functioning properly. For instance, oligonucleotides are used as primers in PCR reactions to detect HIV nucleic acids in biological samples such as human blood in clinical settings. The packaging vector, which comprises nucleic acid subsequences corresponding to the region to be amplified is used as an amplification templates in a separate reaction from a test sample such as human blood to determine that the PCR reagents and hybridization conditions are appropriate. Similarly, the polypeptides encoded by the packaging vector can be used to check ELISA reagents in assays for the detection of HIV expression products in biological samples.

EXAMPLE 20

Cellular Transformation and Gene Therapy

The present invention provides packageable nucleic acids for the transformation of cells *in vitro* and *in vivo*. These packageable nucleic acids are packaged in HIV-2 particles in the packaging cell lines described herein. The nucleic acids are transfected into cells through the interaction of the HIV particle surrounding the nucleic acid and the HIV cellular receptor.

Cells which can be transfected by HIV particles include, but are not limited to: CD4+ cells, including T-cells such as Molt-4/8 cells, SupT1 cells, H9 cells, C8166 cells and myelomonocytic (U937) cells as well as primary human lymphocytes, and primary human monocyte-macrophage cultures, peripheral blood dendritic cells, follicular dendritic cells, epidermal Langerhans cells, megakaryocytes, microglia, astrocytes, oligodendroglia, CD8+ cells, retinal cells, renal epithelial cells, cervical cells, rectal mucosa, trophoblastic cells, and cardiac myocytes. Thus, the packageable nucleic acids of the invention are generally useful as cellular transformation vectors.

In one particular class of embodiments, the packageable nucleic acids of the invention are used in cell transformation procedures for gene therapy. Gene therapy provides methods for combating chronic infectious diseases such as HIV, as well as non-infectious diseases such as cancer and birth defects such as enzyme deficiencies. Yu *et al. Gene Therapy* 1:13-26, 1994, and the references therein provides a general guide to gene therapy strategies for HIV infection. See also, Sodoski et al. PCT/US91/04335. One general limitation of common gene therapy vectors such as murine retroviruses is that they only infect actively dividing cells, and they are generally non-specific. The present invention provides several features that allow one of skill to generate powerful retroviral gene therapy vectors which specifically target cells *in vivo* (for example CD4+ cells), and which transform many cell types *in vitro*. CD4+ cells, including non-dividing cells, are transduced by nucleic acids packaged in HIV particles. HIV particles also infect other cell-types in vitro which exhibit little or no CD4 expression, such as those listed in the preceding paragraph. Thus, these cells can be targeted by the HIV particle-packaged nucleic acids of the invention in ex vivo gene therapy procedures, or in drug discovery assays which require transformation of these cell types.

Pseudotyping the Packageable Vector

Hematopoietic stem cells are targets for cell transformation in general, and for gene therapy in particular. Packageable vectors are made competent to transform CD34+ cells by pseudotyping the vector. This is done by transducing the packaging cell line used to package the vector with a nucleic acid which encodes the vesicular stomatitis virus (VSV) envelope protein, which is expressed on the surface of the vector. VSV infects both dividing and non-dividing CD34+ cells, and pseudotype vectors expressing VSV envelope proteins are competent to transduce these cells.

Similarly, viral or cellular proteins in general can be co-expressed to increase the host range of an HIV-based vector. Typically, a nucleic acid encoding a selected protein is coexpressed in an HIV packaging cell of the invention. Protein encoded by the nucleic acid is incorporated into the particle which packages an HIV-packageable nucleic acid, which buds off from the packaging cell membrane. If the protein is recognized by a cellular receptor on a target cell, the particle is transduced into the cell by receptor mediated endocytosis. Examples of such proteins include viral (such as retroviral) envelope or coat proteins, cell receptor ligands, antibodies or antibody fragments which bind cell receptors on target cells, and the like.

Promoters

One embodiment of the invention can use an HIV LTR sequence as a promoter for the HIV packageable vector. These LTR sequences are trans-activated upon infection of a cell containing the LTR promoter by the infecting virus. LTR promoters, in addition to binding tat

and rev are responsive to cellular cytokines (such as IL-2 and SP-1) which act to permit transcription of the HIV genome upon infection. Thus, in one example, a therapeutic nucleic acid is placed under the control of an LTR promoter, rendering the cells ordinarily most vulnerable to HIV infection resistant to infection. See, e.g., Poznansky et al., *J. Virol.* 65: 532-536, 1991, for a description of the region flanking the 5' LTR's ability to package vector nucleic acids.

Ex Vivo Transformation of Cells

Ex vivo methods for inhibiting viral replication in a cell in an organism involve transducing the cell *ex vivo* with a therapeutic nucleic acid of this invention, and introducing the cell into the organism. The cells are typically CD4+ cells, such as CD4+ T cells or macrophages isolated or cultured from a patient, or are stem cells. Alternatively, the cells can be those stored in a cell bank (e.g., a blood bank). In one embodiment, the packageable nucleic acid encodes an anti-viral therapeutic agent (e.g., suicide gene, trans-dominant gene, anti-HIV ribozyme, anti-sense gene, or decoy gene) which inhibits the growth or replication of an HIV virus, under the control of an activated or constitutive promoter. The cell transformation vector inhibits viral replication in any of those cells already infected with HIV virus, in addition to conferring a protective effect to cells which are not infected by HIV.

In some embodiments, the vector is replicated and packaged into HIV capsids using the HIV replication machinery, thereby causing the anti-HIV therapeutic gene to propagate in conjunction with the replication of an HIV virus. Thus, an organism infected with HIV can be treated for the infection by transducing a population of its cells with a vector of the invention and introducing the transduced cells back into the organism as described herein. Thus, the present invention provides a method of protecting cells *in vitro*, *ex vivo* or *in vivo*, even when the cells are already infected with the virus against which protection is sought.

Stem cells (which are typically not CD4+) can be used in *ex-vivo* procedures for cell transformation and gene therapy. The advantage of using stem cells is that they can be differentiated into other cell types *in vitro*, or can be introduced into a mammal (such as the donor of the cells) where they will engraft in the bone marrow. Methods for differentiating CD34+ cells *in vitro* into clinically important immune cell types using cytokines such a GM-CSF, IFN-γ and TNF-α are known (see, Inaba et al., *J. Exp. Med.* 176:1693-1702, 1992). Methods of pseudotyping HIV-based vectors so that they can transform stem cells are described above.

Stem cells are isolated for transduction and differentiation using known methods. For example, in mice, bone marrow cells are isolated by sacrificing the mouse and cutting the leg bones with a pair of scissors. Stem cells are isolated from bone marrow cells by panning the bone marrow cells with antibodies which bind unwanted cells, such as CD4+ and CD8+ (T cells), CD45+ (panB cells), GR-1 (granulocytes), and Ia^d (differentiated antigen presenting cells). For an example of this protocol see, Inaba et al., *J. Exp. Med.* 176:1693-1702, 1992.

In humans, bone marrow aspirations from iliac crests are performed e.g., under general anesthesia in the operating room. The bone marrow aspirations are collected from the posterior iliac bones and crests. If the total number of cells collected is $< 2 \times 10^8$/kg, a second aspiration using the sternum and anterior iliac crests in addition to posterior crests is performed. During the operation, two units of irradiated packed red cells are administered to replace the volume of marrow taken by the aspiration. Human hematopoietic progenitor and stem cells are characterized by the presence of a CD34 surface membrane antigen. This antigen is used for purification, e.g., on affinity columns which bind CD34.

After the bone marrow is harvested, the mononuclear cells are separated from the other components by means of ficol gradient centrifugation. This is performed by a semi-automated method using a cell separator (e.g., a Baxter Fenwal CS3000+ or Terumo machine). The light density cells, composed mostly of mononuclear cells are collected and the cells are incubated in plastic flasks at 37° C for 1.5 hours. The adherent cells (monocytes, macrophages and B-Cells) are discarded. The non-adherent cells are then collected and incubated with a monoclonal anti-CD34 antibody (e.g., the murine antibody 9CS) at 4°C for 30 minutes with gentle rotation. The final concentration for the anti-CD34 antibody is 10 μg/ml. After two washes, paramagnetic microspheres (Dyne Beads, supplied by Baxter Immunotherapy Group, Santa Ana, California) coated with sheep antimouse IgG (Fc) antibody are added to the cell suspension at a ratio of 2 cells/bead. After a further incubation period of 30 minutes at 4°C, the rosetted cells with magnetic beads are collected with a magnet. Chymopapain (supplied by Baxter Immunotherapy Group, Santa Ana, California) at a final 5 concentration of 200 U/ml is added to release the beads from the CD34+ cells. Alternatively, an affinity column isolation procedure can be used which binds to CD34, or to antibodies bound to CD34 (see, the examples below). See, Ho et al., *Stem Cells* 13 (suppl. 3): 100-105, 1995. See also, Brenner, *J. Hematotherapy* 2: 7-17, 1993.

In another embodiment, hematopoetic stem cells are isolated from fetal cord blood. Yu et al., *PNAS USA* 92: 699-703, 1995, describes another method of transducing CD34+ cells from human fetal cord blood using retroviral vectors.

Ex vivo transformation of T cells

Rather than using stem cells, T cells are also used in other examples of *ex vivo* procedures. Several techniques are known for isolating T cells. In one method, Ficoll-Hypaque density gradient centrifugation is used to separate PBMC from red blood cells and neutrophils according to established procedures. Cells are washed with modified AIM-V [which consists of AIM-V (GIBCO) with 2 mM glutamine, 10 μg/ml gentamicin sulfate, 50 μg/ml streptomycin) supplemented with 1% fetal bovine serum (FBS)]. Enrichment for T cells is performed by negative or positive selection with appropriate monoclonal antibodies coupled to columns or

magnetic beads according to standard techniques. An aliquot of cells is analyzed for desired cell surface phenotype (e.g., CD4, CD8, CD3, CD14, etc.).

Cells are washed and resuspended at a concentration of 5 x 10^5 cells per ml of AIM-V modified as above and containing 5% FBS and 100 U/ml recombinant IL-2 (rIL-2) (supplemented AIM-V). Where the cells are isolated from an HIV^+ patient, 25 nM CD4-PE40 (a recombinant protein consisting of the HIV-1-binding CD4 domain linked to the translocation and ADP-ribosylation domains of Pseudomonas aeruginosa exotoxin A) is optionally added to the cell cultures for the remainder of the cell expansion to selectively remove HIV infected cells from the culture. CD4-PE40 has been shown to inhibit p24 production in HIV-1-infected cell cultures and to selectively kill HIV-1-infected cells.

To stimulate proliferation, OKT3 monoclonal antibody (Ortho Diagnostics) is added to a concentration of 10 ng/ml and the cells are plated in 24 well plates with 0.5 ml per well. The cells are cultured at 37°C in a humidified incubator with 5% CO2 for 48 hours. Media is aspirated from the cells and 1 ml of vector-containing supernatant (described below) supplemented with 5 pl/ml of protamine sulfate, 100 U/ml rIL-2, 100 U/ml penicillin, 0.25 μg/ml amphotericin B/ml, and an additional 100 μg/ml streptomycin (25 nM CD4-PE40 can be added as described above).

The expression of surface markers facilitates identification and purification of T cells. Methods of identification and isolation of T cells include fluorescence activated cell sorting (FACS), column chromatography, panning with magnetic beads, western blots, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, and the like, and various immunological methods such as fluid or gel precipitin reactions, inununodiffusion (single or double), immunonoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, and the like. For a review of immunological and immunoassay procedures in general, see Stites and Terr (eds.) 1991 Basic and Clinical Immunology (7th ed). For a discussion of how to make antibodies to selected antigens see, e.g. Coligan (1991) Current Protocols in Immunology Wiley/Greene, NY; and Harlow and Lane (1989) Antibodies: A Laboratory Manual Cold Spring Harbor Press, NY; Stites et al. (eds.) Basic and Clinical Immunology (4th ea.)

In addition to the *ex vivo* uses described above, the packaging cell lines of the invention and the HIV packageable nucleic acids of the invention are useful generally in cloning methods. Packageable nucleic acids are packaged in an HIV particle and used to transform an HIV-infectible cell (e.g., a CD4+ cell) *in vitro* or *in vivo*. This provides one of skill with a technique for transforming cells with a nucleic acid of choice, e.g., in drug discovery assays, or as a tool in the study of gene regulation.

In Vivo Transformation

HIV particles containing therapeutic nucleic acids can be administered directly to the organism for transduction of cells *in vivo*. Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells. The packaged nucleic acids are administered in any suitable manner, preferably with pharmaceutically acceptable carriers. Suitable methods of administering such packaged nucleic acids in the context of the present invention to a patient are available, and although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route.

Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention, some of which are reviewed in PCT/US97/05272 (also see EXAMPLE 22).

The packaged nucleic acids are not freeze-dried (lyophilized) because HIV particles are destroyed by lyophilization. Injection solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. Cells transduced by the packaged nucleic acid as described above in the context of *ex vivo* therapy can also be administered intravenously or parenterally as described above. The dose administered to a subject, in the context of the present invention should be sufficient to effect a beneficial therapeutic response in the patient over time, or to inhibit infection by a pathogen. The dose will be determined by the efficacy of the particular vector employed and the condition of the patient, as well as the body weight or surface area of the subject to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular vector, or transduced cell type in a particular patient.

In determining the effective amount of the vector to be administered in the treatment of a disease, the physician or other clinician evaluates circulating plasma levels, vector toxicities, progression of the disease, and the production of anti-vector antibodies. In general, the dose equivalent of a naked nucleic acid from a vector is from about 1 μg to 100 μg for a typical 70 kilogram patient, and doses of vectors which include a retroviral particle are calculated to yield an equivalent amount of inhibitor nucleic acid.

For administration, inhibitors and transduced cells of the present invention can be administered at a rate determined by the LD-50 of the inhibitor, vector, or transduced cell type, and the side-effects of the inhibitor, vector or cell type at various concentrations, as applied to the mass and overall health of the patient. Administration can be accomplished via single or divided doses.

Prior to infusion, blood samples are obtained and saved for analysis. Between 1×10^8 and 1×10^{12} transduced cells are infused intravenously over 60-200 minutes. Leukopheresis,

transduction and reinfusion are repeated every 2 to 3 months for a total of 4 to 6 treatments in a one year period.

Transduced cells are prepared for reinfusion according to established methods. See, Abrahamsen et al., *J. Clin. Apheresis* 6:48-53, 1991; Carter et al. *J. Clin. Arpheresis* 4:113-117, 1988; Aebersold et al., *J. Immunol. Methods* 112: 1-7, 1988; Muul et al., *J. Immunol. Methods* 101: 171-181, 1987; and Carter et al., *Transfusion* 27:362-365, 1987. After a period of about 24 weeks in culture, the cells should number between 1 x 10^8 and 1 x 10^{12}. In this regard, the growth characteristics of cells vary from patient to patient and from cell type to cell type. About 72 hours prior to reinfusion of the transduced cells, an aliquot is taken for analysis of phenotype, and percentage of cells expressing the therapeutic agent.

EXAMPLE 21

Sequence Variants

Having presented the nucleotide sequence of several lentiviral packaging and transfer vectors, as well as several therapeutic transgenes, this invention now also facilitates the creation and use of DNA molecules, and thereby proteins, which are derived from those disclosed but which vary in their precise nucleotide or amino acid sequence from those disclosed or those sequences which can be used as transgenes. Such variants can be obtained through a combination of standard molecular biology laboratory techniques and the nucleotide sequence information disclosed by this invention.

Variant DNA molecules include those created by standard DNA mutagenesis techniques, for example, M13 primer mutagenesis. Details of these techniques are provided in Sambrook et al. (In: Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989, Ch. 15). By the use of such techniques, variants can be created which differ in minor ways from those disclosed. DNA molecules and nucleotide sequences which are derivatives of those specifically disclosed herein and which differ from those disclosed by the deletion, addition or substitution of nucleotides while still encoding a protein which possesses the functional characteristics of the lentiviral and/or transgene proteins are comprehended by this invention.

Also within the scope of this invention are small DNA molecules which are derived from the disclosed DNA molecules. Such small DNA molecules include oligonucleotides suitable for use as hybridization probes or PCR primers. As such, these small DNA molecules will comprise at least a segment of the lentiviral or transgene DNA molecules and for the purposes of PCR, will comprise at least a 20-50 nucleotide sequence of the lentiviral or transgene DNA or gene (i.e., at least 20-50 consecutive nucleotides of the lentiviral or transgene DNA or gene sequences). DNA molecules and nucleotide sequences which are derived from the disclosed DNA molecules as described above can also be defined as DNA sequences which hybridize under stringent conditions to the DNA sequences disclosed, or fragments thereof.

Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of the hybridization method of choice and the composition and length of the hybridizing DNA used. Generally, the temperature of hybridization and the ionic strength (especially the Na^+ concentration) of the hybridization buffer will determine the stringency of hybridization. Calculations regarding hybridization conditions required for attaining particular degrees of stringency are discussed by Sambrook et al. (In: Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989 ch. 9 and 11), herein incorporated by reference. By way of illustration only, a hybridization experiment can be performed by hybridization of a DNA molecule (for example, a deviation of the AADC cDNA) to a target DNA molecule (for example, the AADC cDNA) which has been electrophoresed in an agarose gel and transferred to a nitrocellulose membrane by Southern blotting (Southern, *J. Mol. Biol.* 98:503, 1975), a technique well known in the art and described in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989).

Hybridization with a target probe labeled with [^{32}P]-dCTP is generally carried out in a solution of high ionic strength such as 6xSSC at a temperature that is 20-25°C below the melting temperature, T_m, described below. For such Southern hybridization experiments where the target DNA molecule on the Southern blot contains 10 ng of DNA or more, hybridization is typically carried out for 6-8 hours using 1-2 ng/ml radiolabeled probe (of specific activity equal to 10^9 CPM/μg or greater). Following hybridization, the nitrocellulose filter is washed to remove background hybridization. The washing conditions should be as stringent as possible to remove background hybridization but to retain a specific hybridization signal. The term T_m represents the temperature above which, under the prevailing ionic conditions, the radiolabeled probe molecule will not hybridize to its target DNA molecule. The T_m of such a hybrid molecule can be estimated from the following equation (Bolton and McCarthy, *Proc. Natl. Acad. Sci. USA* 48:1390, 1962): $T_m = 81.5°C - 16.6(\log_{10}[Na^+]) + 0.41(\%G+C) - 0.63(\%\ \text{formamide}) - (600/l)$; where l = the length of the hybrid in base pairs.

This equation is valid for concentrations of Na^+ in the range of 0.01 M to 0.4 M, and it is less accurate for calculations of T_m in solutions of higher $[Na^+]$. The equation is also primarily valid for DNAs whose G+C content is in the range of 30% to 75%, and it applies to hybrids greater than 100 nucleotides in length (the behavior of oligonucleotide probes is described in detail in Ch. 11 of Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989).

Thus, by way of example, for a 150 base pair DNA probe derived from the open reading frame of the AADC cDNA (with a hypothetical %GC = 45%), a calculation of hybridization conditions required to give particular stringencies can be made as follows: For this example, it is assumed that the filter will be washed in 0.3 xSSC solution following hybridization, thereby: $[Na^+] = 0.045$ M; %GC = 45%; Formamide concentration = 0; l = 150 base pairs; $T_m = 81.5 - 16.6(\log_{10}[Na^+]) + (0.41 \times 45) - (600/150)$; and so $T_m = 74.4°C$.

The T_m of double-stranded DNA decreases by 1-1.5°C with every 1% decrease in homology (Bonner et al., *J. Mol. Biol.* 81:123, 1973). Therefore, for this given example, washing the filter in 0.3 xSSC at 59.4-64.4°C will produce a stringency of hybridization equivalent to 90%; that is, DNA molecules with more than 10% sequence variation relative to the target cDNA (for example AADC) will not hybridize. Alternatively, washing the hybridized filter in 0.3 xSSC at a temperature of 65.4-68.4°C will yield a hybridization stringency of 94%; that is, DNA molecules with more than 6% sequence variation relative to the target cDNA molecule (for example AADC) will not hybridize. The above example is given entirely by way of theoretical illustration. One skilled in the art will appreciate that other hybridization techniques can be utilized and that variations in experimental conditions will necessitate alternative calculations for stringency.

In particular embodiments of the present invention, stringent conditions can be defined as those under which DNA molecules with more than 25%, 15%, 10%, 6% or 2% sequence variation (also termed "mismatch") will not hybridize.

The degeneracy of the genetic code further widens the scope of the present invention as it enables major variations in the nucleotide sequence of a DNA molecule while maintaining the amino acid sequence of the encoded protein. For example, alanine is encoded in the cDNA by the nucleotide codon triplet GCA. However, because of the degeneracy of the genetic code, three other nucleotide codon triplets, GCT, GCG and GCC, also code for alanine. Thus, the nucleotide sequence of a cDNA could be changed at the alanine position to any of these three codons without affecting the amino acid composition of the encoded protein or the characteristics of the protein. Based upon the degeneracy of the genetic code, variant DNA molecules can be derived from the cDNA molecules disclosed herein using standard DNA mutagenesis techniques as described above, or by synthesis of DNA sequences. DNA sequences which do not hybridize under stringent conditions to the cDNA sequences disclosed by virtue of sequence variation based on the degeneracy of the genetic code are herein also comprehended by this invention.

The invention also includes DNA sequences that are substantially identical to any of the DNA sequences disclosed herein, where substantially identical means a sequence that has identical nucleotides in at least 75%, 80%, 85%, 90%, 95% or 98% of the aligned sequences.

One skilled in the art will recognize that the DNA mutagenesis techniques described above can be used not only to produce variant DNA molecules, but will also facilitate the production of proteins which differ in certain structural aspects from the lentiviral or transgene proteins, yet which proteins are clearly derivative of this protein and which maintain the essential characteristics of the lentiviral or transgene protein. Newly derived proteins can also be selected in order to obtain variations on the characteristic of the lentiviral or transgene protein, as will be more fully described below. Such derivatives include those with variations in amino acid sequence including minor deletions, additions and substitutions.

While the site for introducing an amino acid sequence variation is predetermined, the

mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis can be conducted at the target codon or region and the expressed protein variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence as described above are well known.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. Deletions or insertions can be made in adjacent pairs, i.e., a deletion of 2 residues or insertion of 2 residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a final construct. Obviously, the mutations that are made in the DNA encoding the protein must not place the sequence out of reading frame and ideally will not create complementary regions that could produce secondary mRNA structure.

Substitutional variants are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made conservatively, as defined above.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those defined above, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histadyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Substitutions of the lentiviral or transgene amino acid sequence can be made either in regions that are highly conserved between species, or regions that share less conservation between species.

The effects of these amino acid substitutions or deletions or additions can be assessed for derivatives of the lentiviral or transgene protein by assays in which DNA molecules encoding the derivative proteins are introduced into the packaging or transfer vector using routine procedures. These vectors would be used to transform cells as described in EXAMPLES 1-14, and analyzed for their ability to allow expression (for example by monitoring the viral titer) of the transgene within the transfer vector.

EXAMPLE 22

Pharmaceutical Compositions and Modes of Administration

Various delivery systems for administering the combined lentiviral therapy of the present invention are known, and include e.g., encapsulation in liposomes, microparticles, microcapsules, receptor-mediated endocytosis (see Wu and Wu, *J. Biol. Chem.* 1987, 262:4429-32). Methods of introduction include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, and oral routes. The compounds can be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and can be administered together with other biologically active agents. Administration can be systemic or local. In addition, the pharmaceutical compositions can be introduced into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection can be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir.

In one embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment, for example, by local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, through a catheter, by a suppository or an implant, such as a porous, non-porous, or gelatinous material, including membranes, such as silastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

The use of liposomes as a delivery vehicle is one delivery method of interest. The liposomes fuse with the target site and deliver the contents of the lumen intracellularly. The liposomes are maintained in contact with the target cells for a sufficient time for fusion to occur, using various means to maintain contact, such as isolation and binding agents. Liposomes can be prepared with purified proteins or peptides that mediate fusion of membranes, such as Sendai virus or influenza virus. The lipids can be any useful combination of known liposome forming lipids, including cationic lipids, such as phosphatidylcholine. Other potential lipids include neutral lipids, such as cholesterol, phosphatidyl serine, phosphatidyl glycerol, and the like. For preparing the liposomes, the procedure described by Kato et al. (*J. Biol. Chem.* 1991, 266:3361) can be used.

The present invention also provides pharmaceutical compositions which include a therapeutically effective amount of the lentiviral vectors, alone or with a pharmaceutically acceptable carrier.

Delivery systems

Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The carrier and composition can be sterile, and the

formulation suits the mode of administration. The composition can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulations can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, and magnesium carbonate.

The amount of the inducing agent and disrupting agent that will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* assays can optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. Effective doses can be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. Instructions for use of the composition can also be included.

The pharmaceutical compositions or methods of treatment can be administered in combination with other therapeutic treatments, such as other antineoplastic or antitumorigenic therapies.

Any of the common pharmaceutical carriers, such as sterile saline solution or sesame oil, can be used. The medium can also contain conventional pharmaceutical adjunct materials such as, for example, pharmaceutically acceptable salts to adjust the osmotic pressure, buffers, preservatives and the like. Other media that can be used in the present invention are normal saline and sesame oil.

Embodiments of the invention comprising medicaments can be prepared with conventional pharmaceutically acceptable carriers, adjuvants and counterions as would be known to those of skill in the art.

The lentiviral vectors of the present invention are administered in an amount effective to produce a therapeutic effect in a subject. The exact dosage of letiviral particles to be administered is dependent upon a variety of factors, including the age, weight, and sex of the subject to be treated, and the nature and extent of the disease or disorder to be treated. The lentiviral particles can be administered as part of a preparation having a titer of lentiviral particles of at least 1×10^{10} pfu/ml, and in general not exceeding 2×10^{11} pfu/ml. The lentiviral particles can be administered

in combination with a pharmaceutically acceptable carrier in a volume up to 10 ml. The pharmaceutically acceptable carrier can be, for example, a liquid carrier such as a saline solution, protamine sulfate (Elkins-Sinn,, Inc., Cherry Hill, N.J.), or Polybrene (Sigma Chemical) as well as others described herein.

Having illustrated and described the principles of generating several different lentiviral transforming and packaging vectors for use in the delivery of therapeutic transgenes to a subject, the art of the invention can be modified in arrangement and detail without departing from such principles. In view of the many possible embodiments to which the principles of my invention can be applied, it should be recognized that the illustrated embodiments are only examples of the invention and should not be taken as a limitation on the scope of the invention. Rather, the scope of the invention is in accord with the following claims. I therefore claim as my invention all that comes within the scope and spirit of these claims.